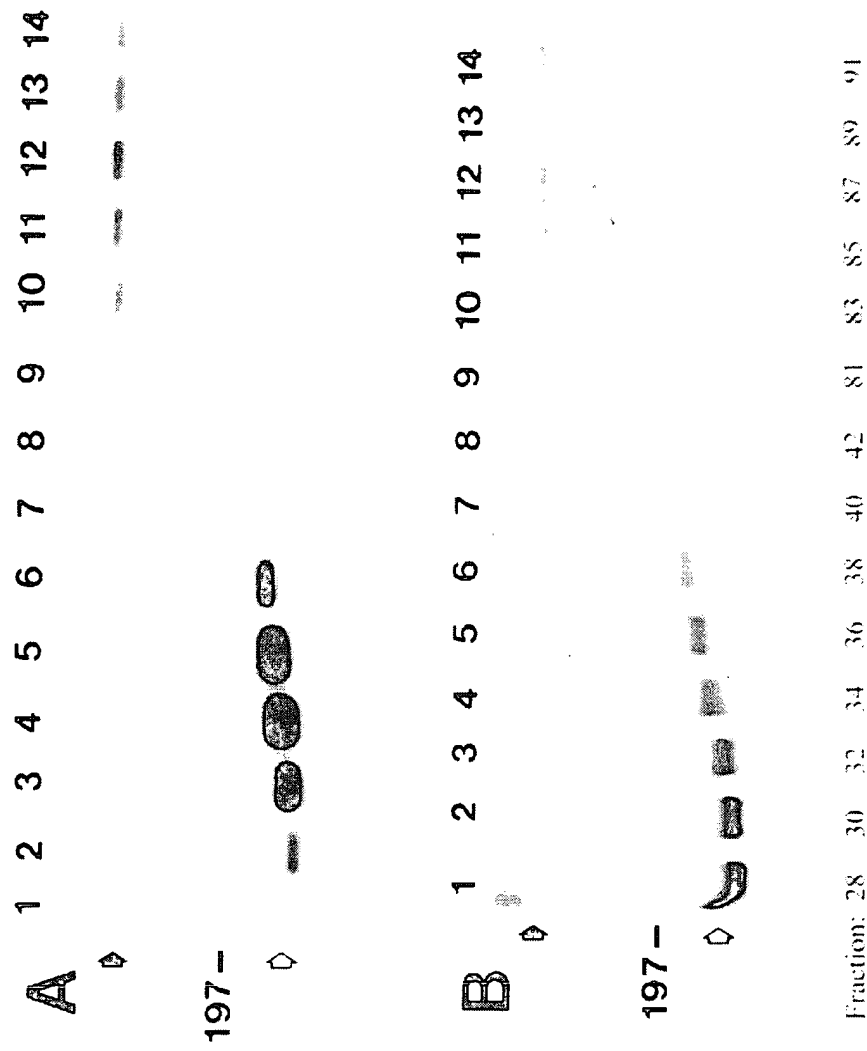
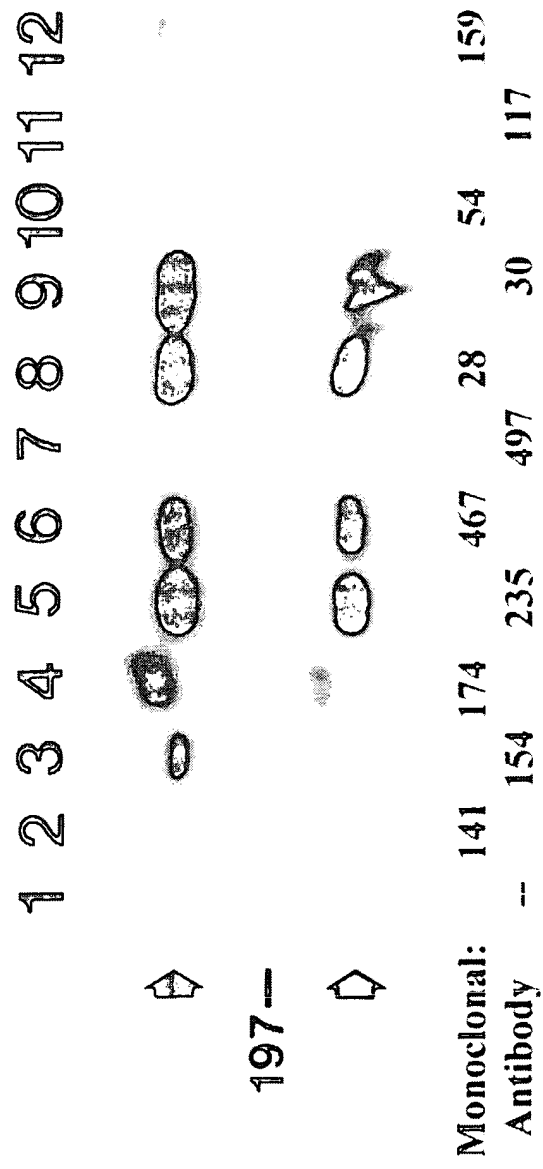


Figure 1



105240" 0E624860

Figure 2



094930.0430
T05240" 0E624860

Figure 3

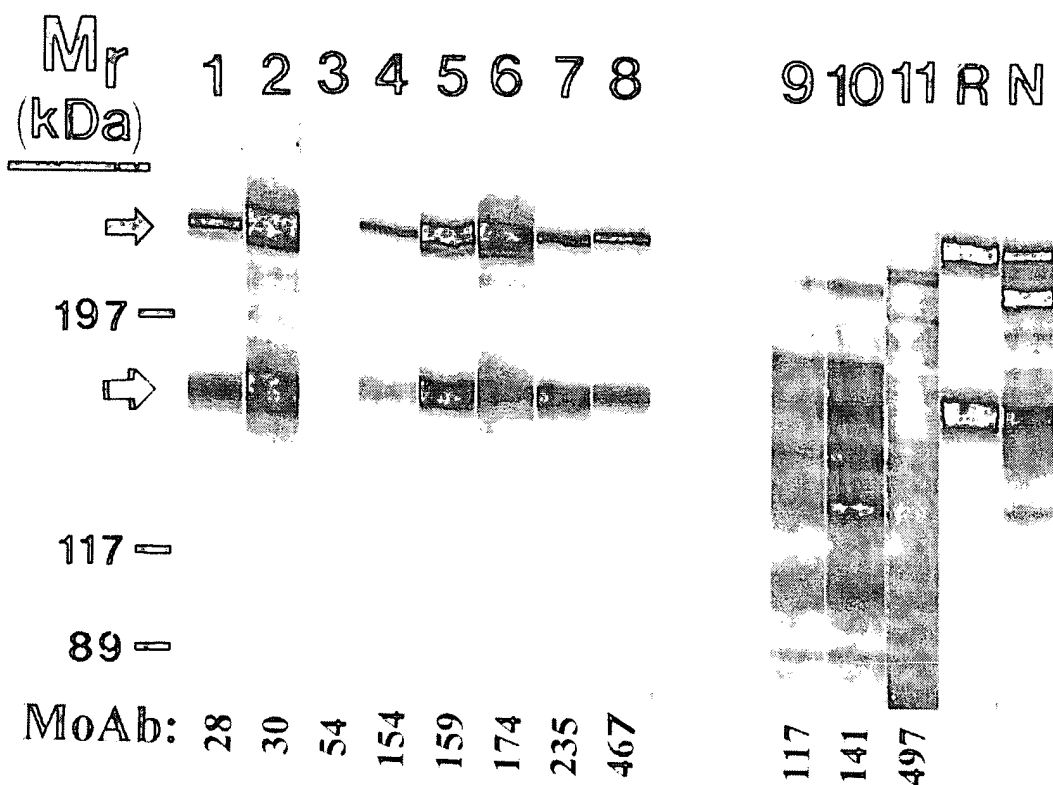
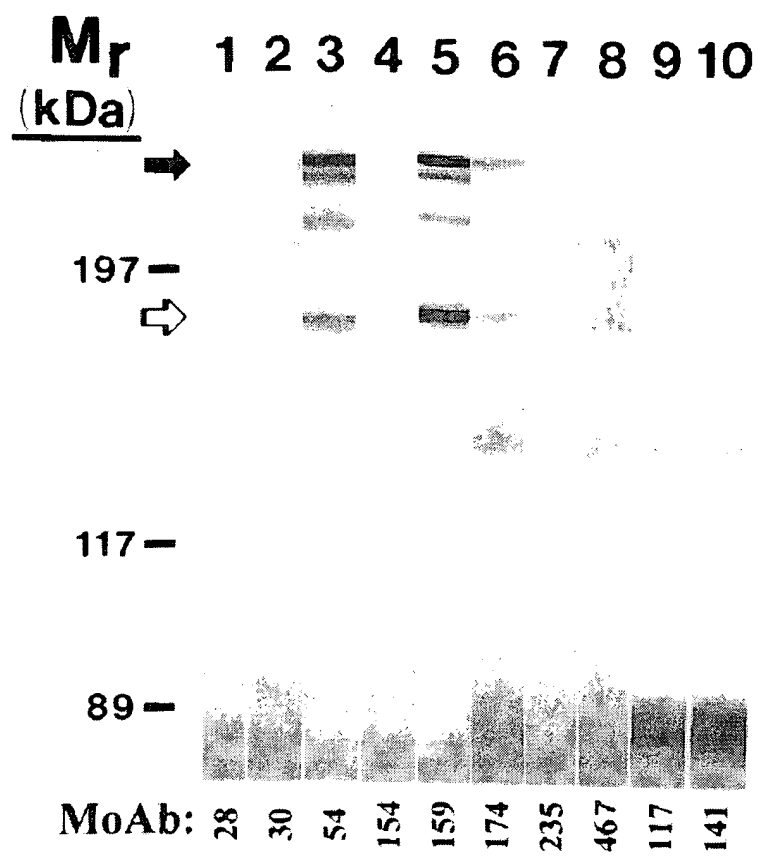
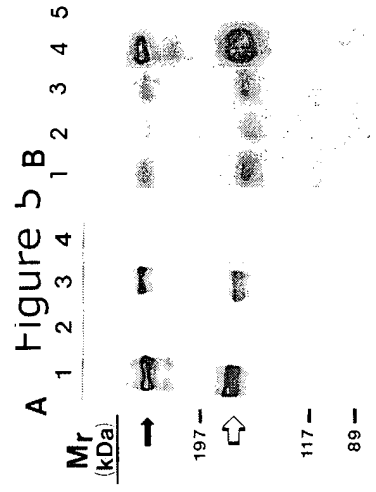


Figure 4



T05240-0E624860



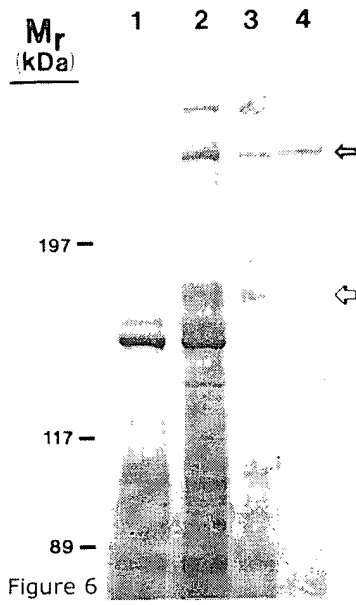
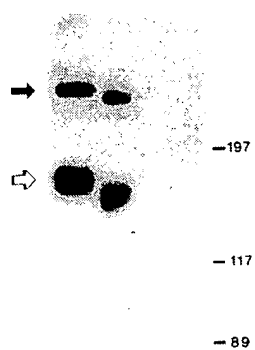


Figure 6

Figure 7 1 2 3 4



PNGaseF:	-	+	-	+
β-ME:	-	-	+	+

Figure 8A

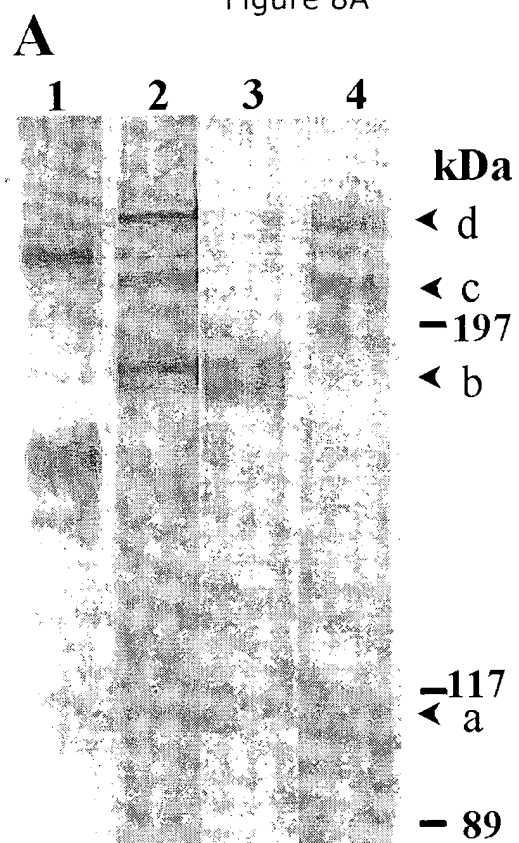
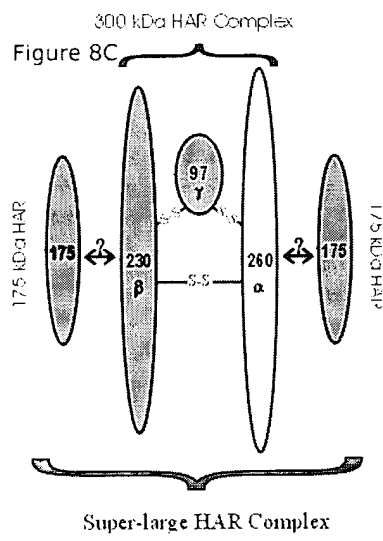


Figure 8B





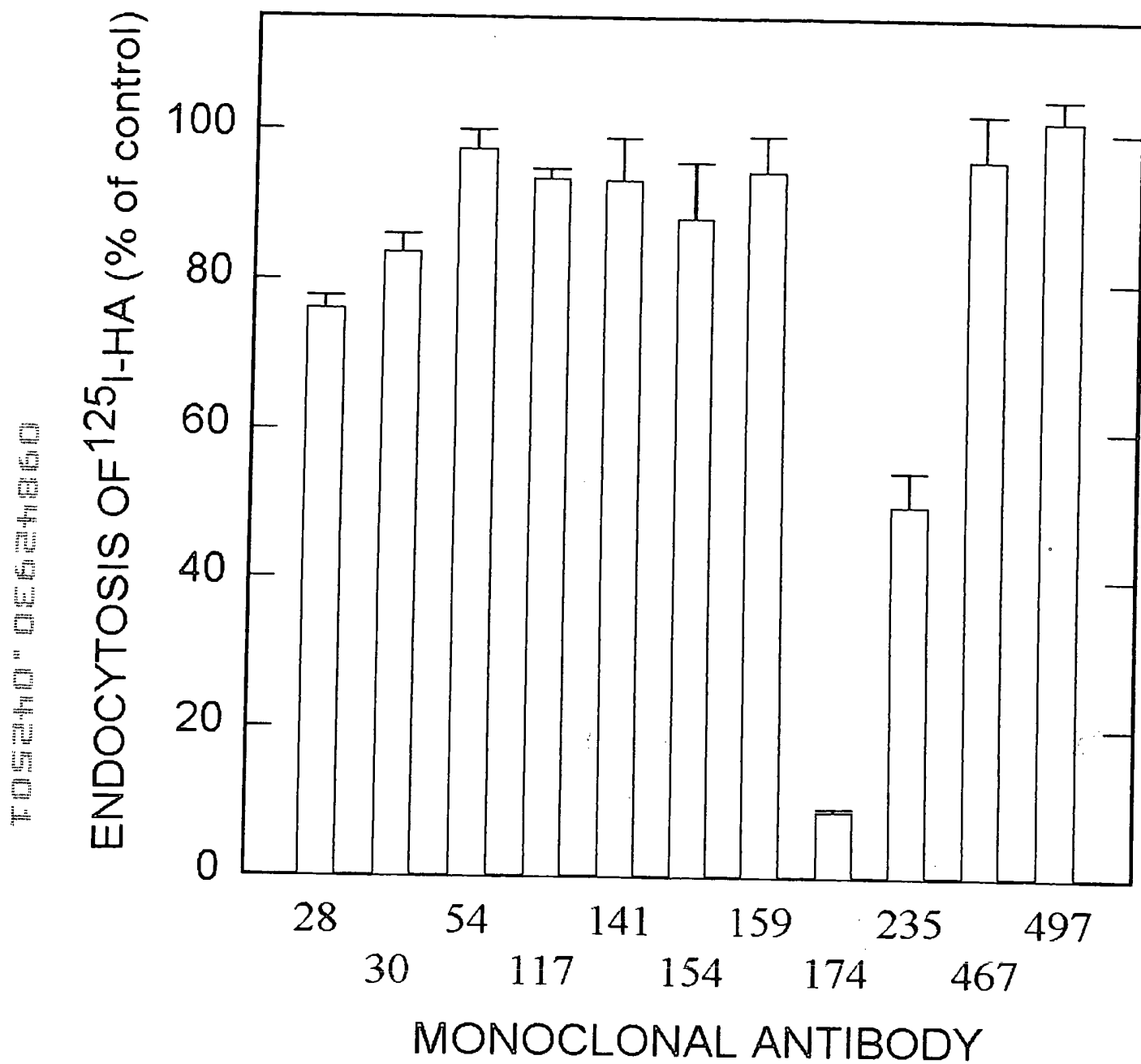
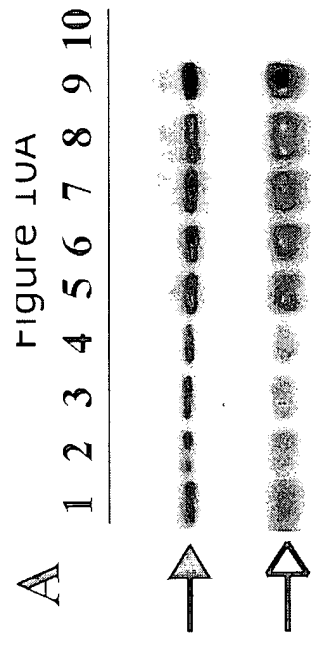


Figure 9



105240" 0E624860

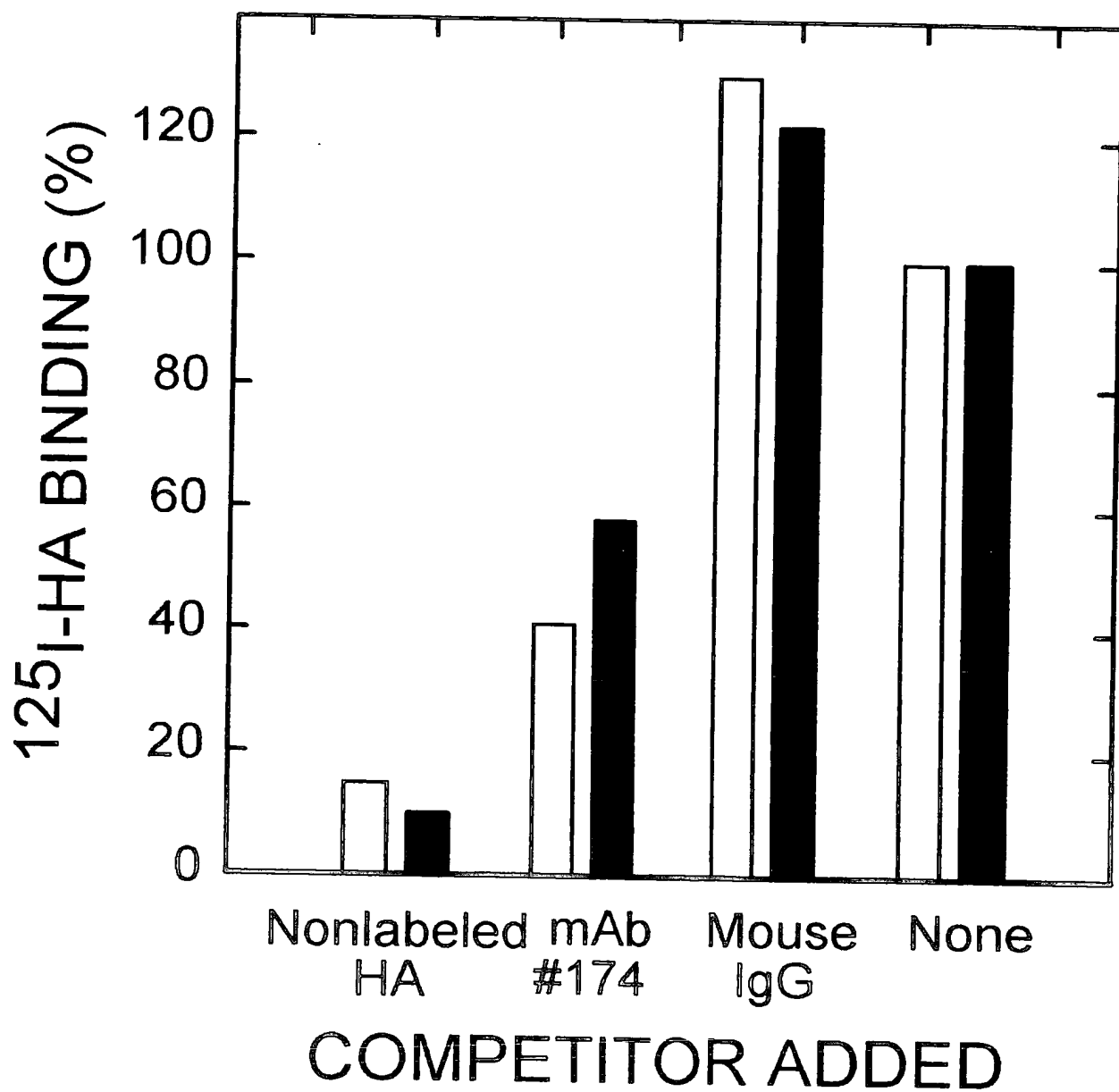


Figure 10B

Figure 11

Antibody Inhibition of HA
Endocytosis by HARE in LECs

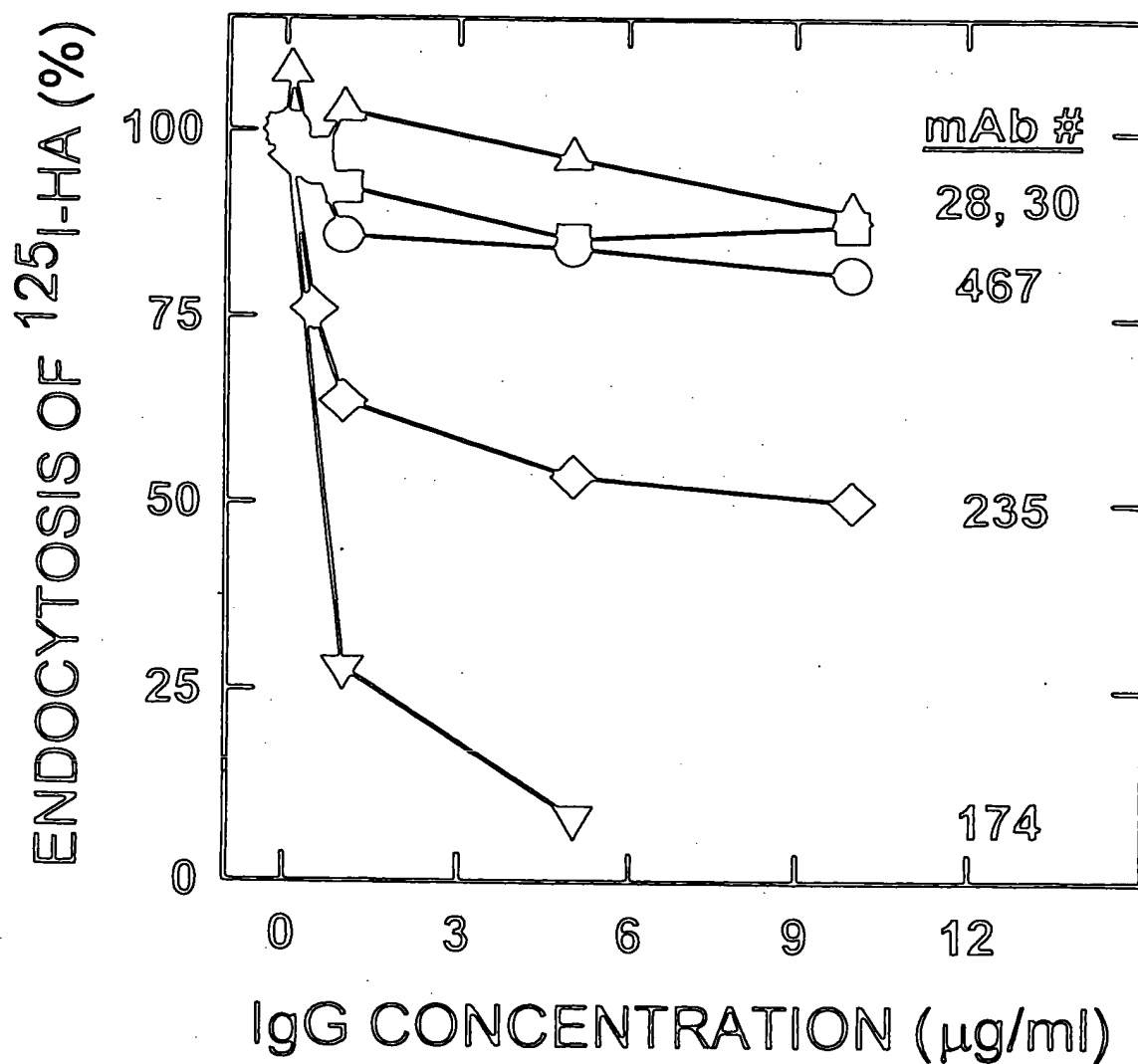


Figure 12

Antibody Inhibition of HA Binding to HARE on LECs is Temperature Dependent

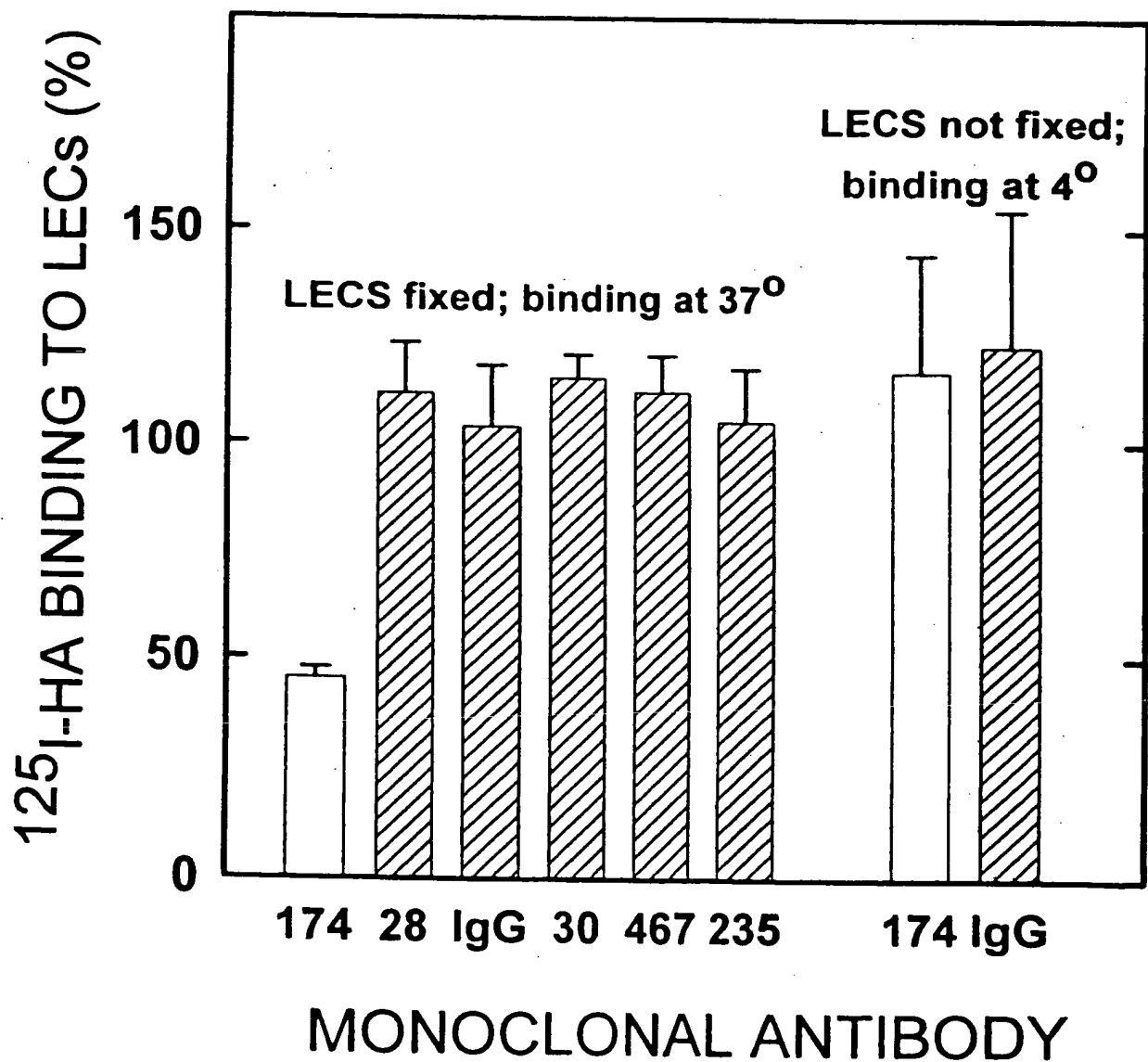
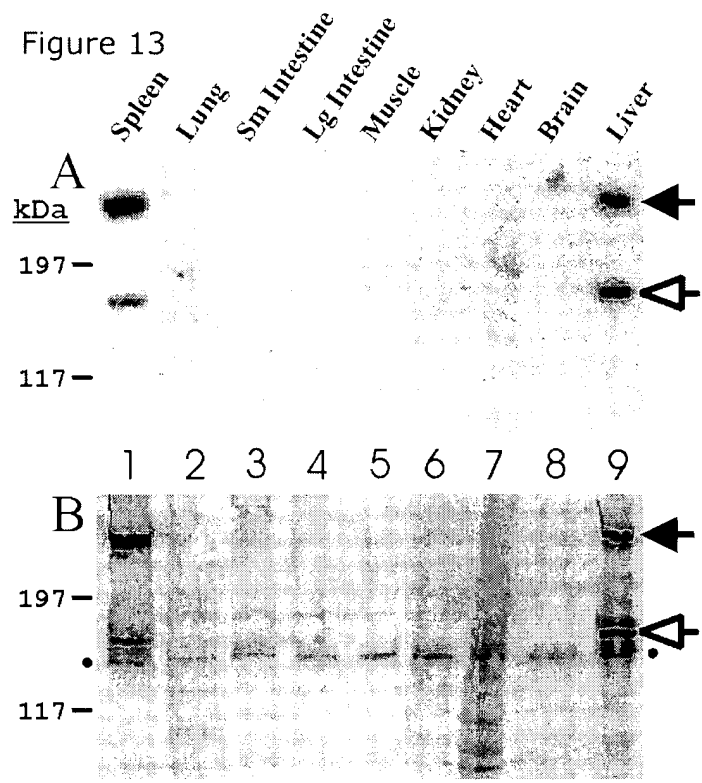


Figure 13



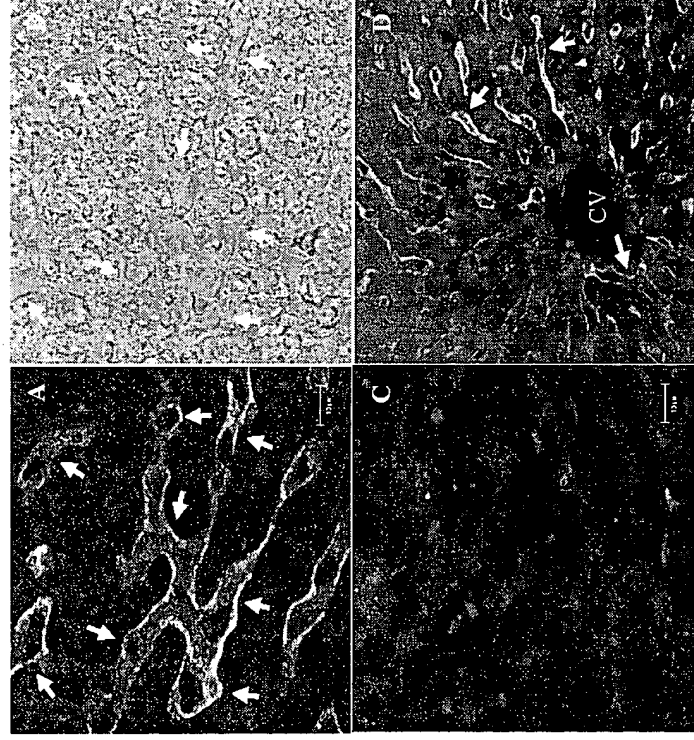


Figure 14

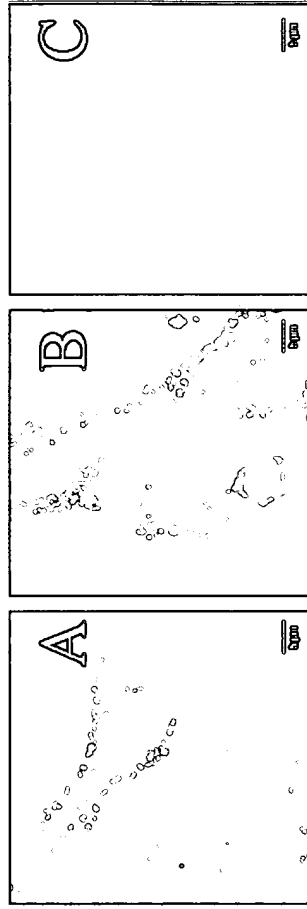


Figure 15

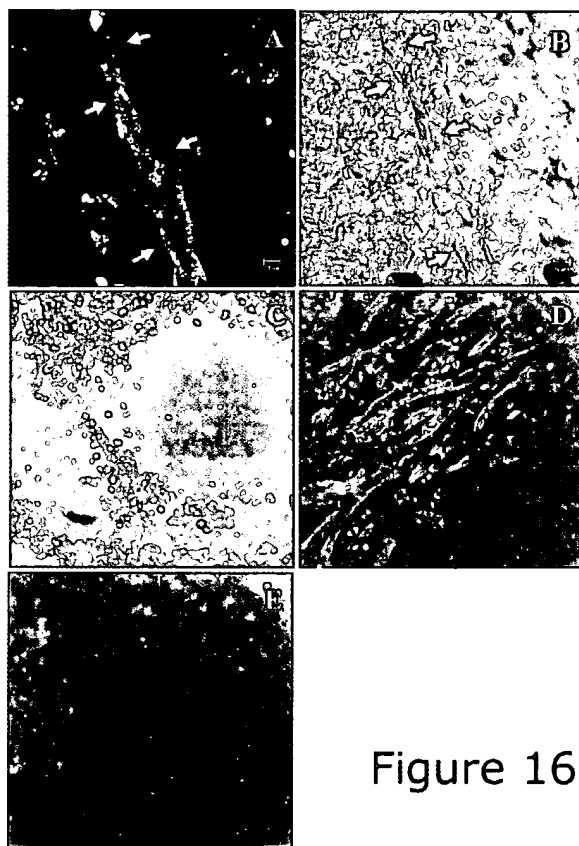


Figure 16

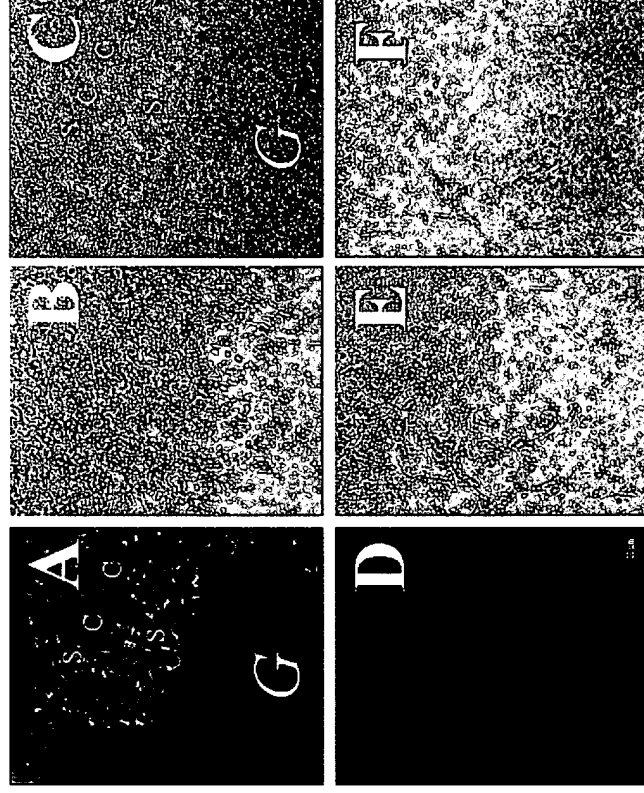
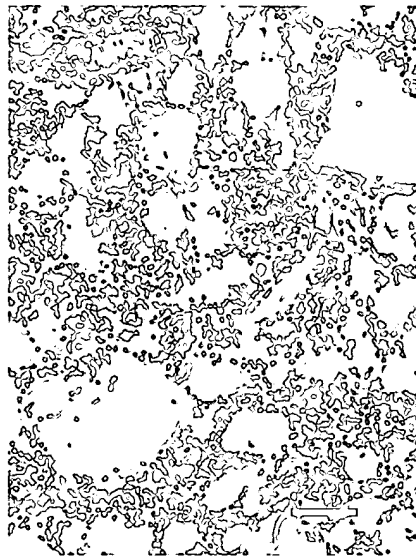
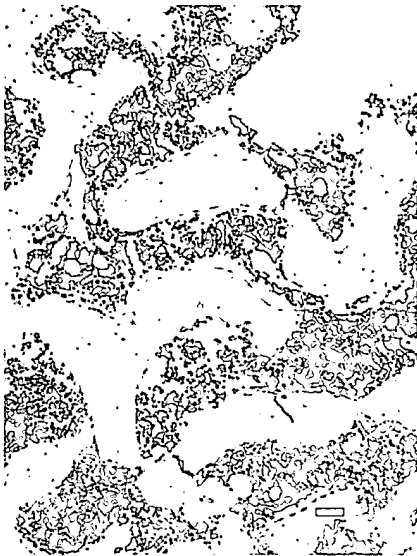


Figure 17

Figure 18

Immunolocalization of HARE
in Bone Marrow

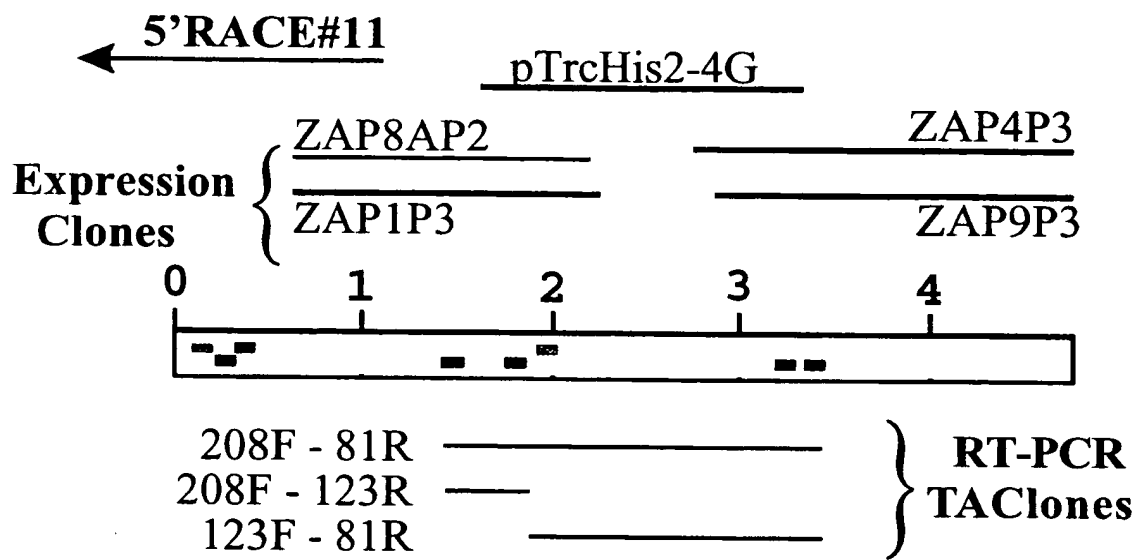
Control



Bars = 50 μ m

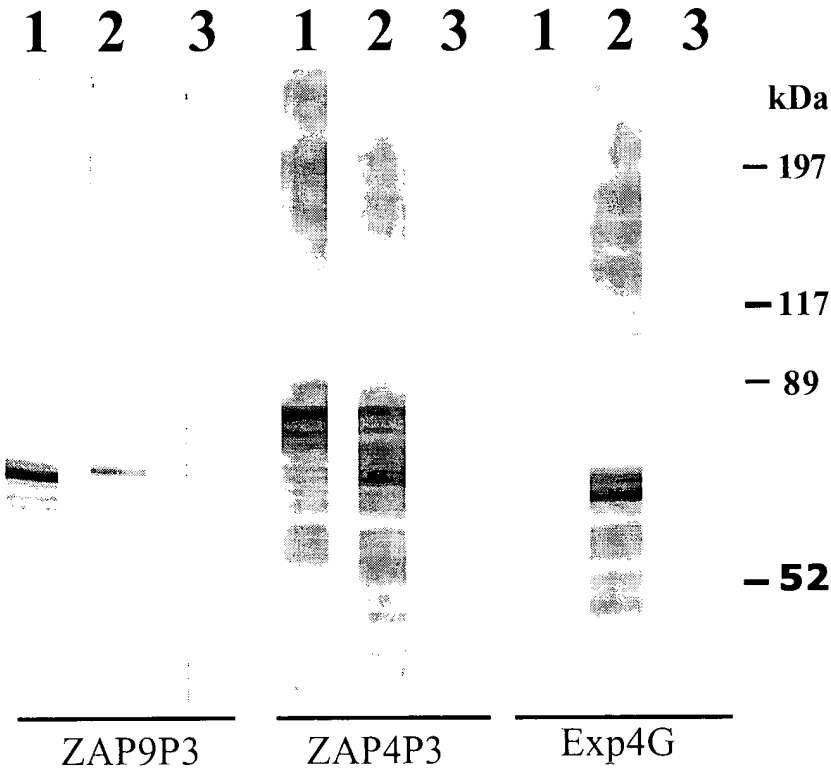
FO5240"0E624860

Figure 19



09842930-042501

Figure 20



09842930-042501

[illegible]

Figure 22

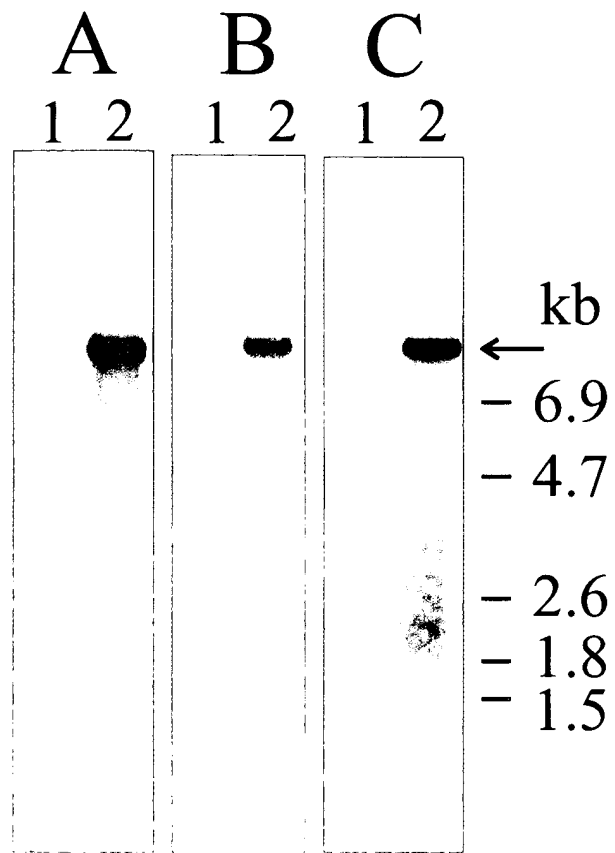


Figure 24

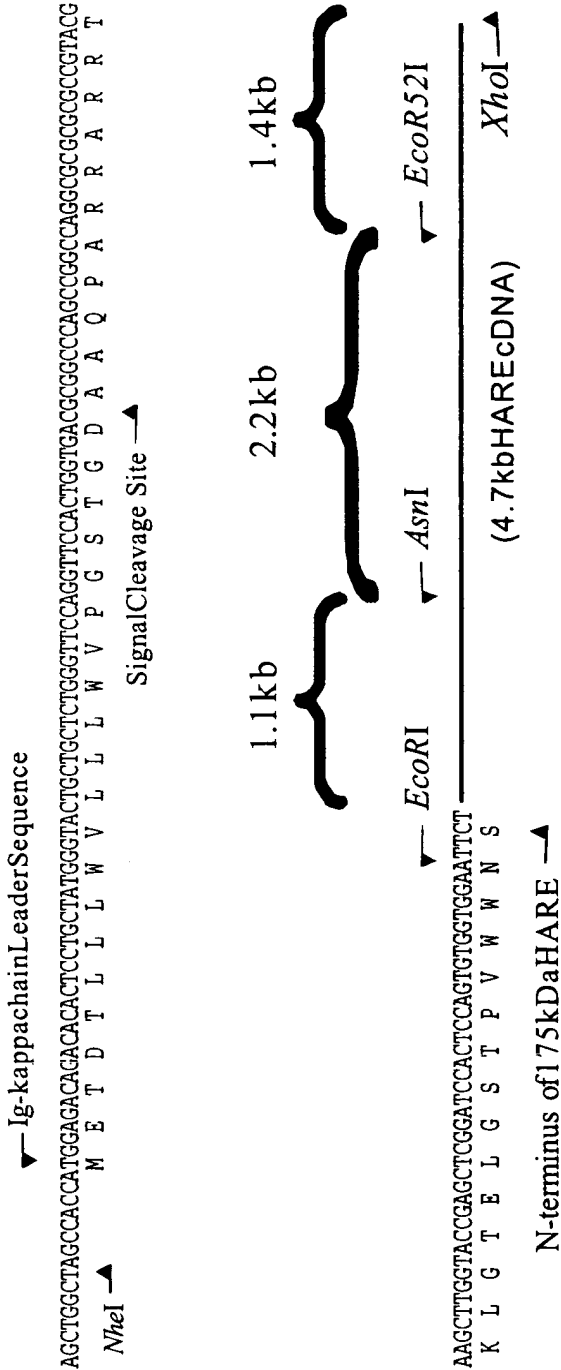


Figure 25

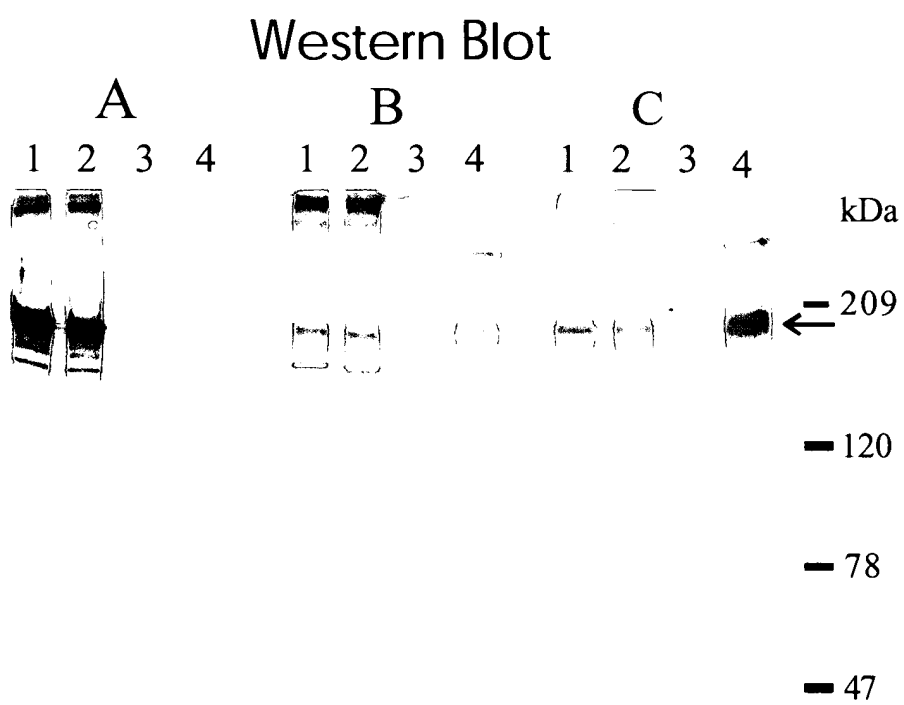
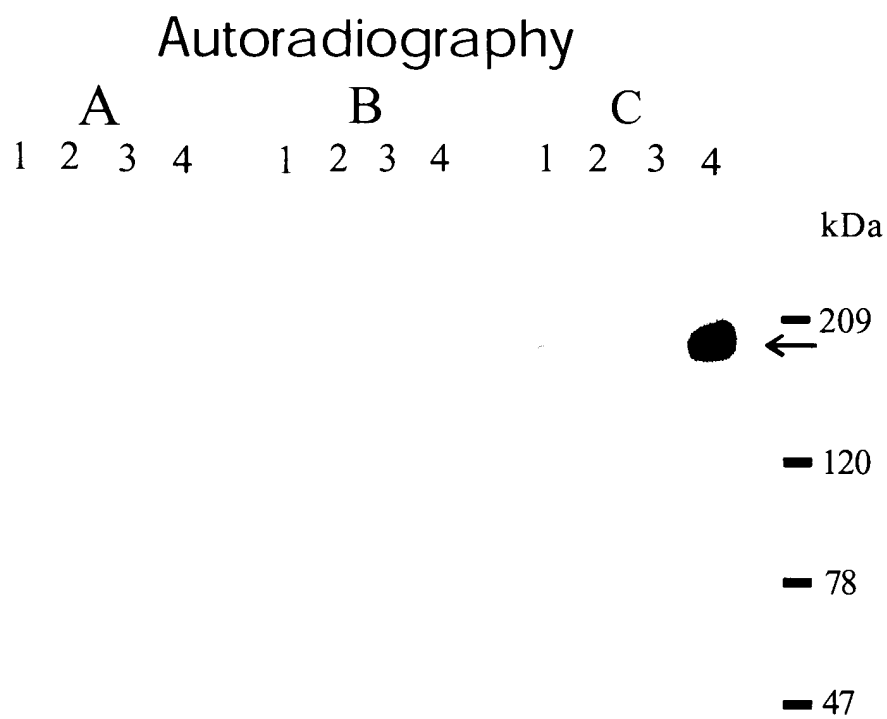
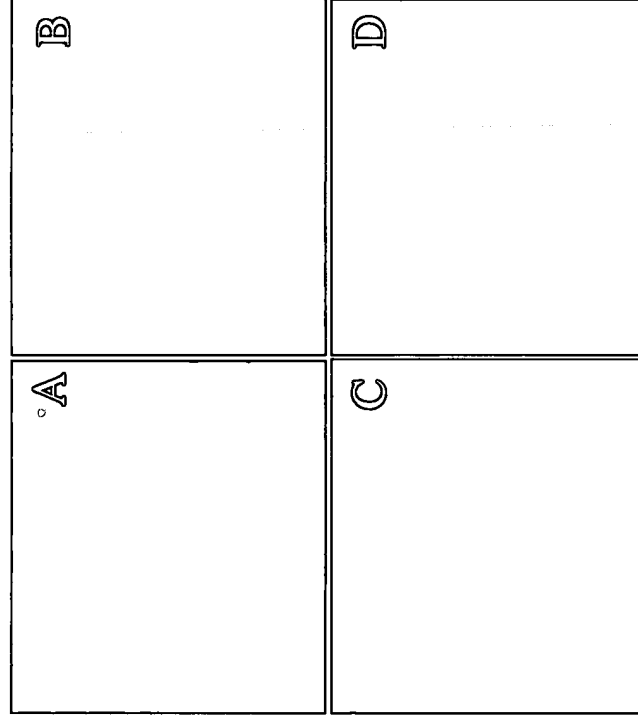


Figure 26



FOI 240 00524860

Figure 27A

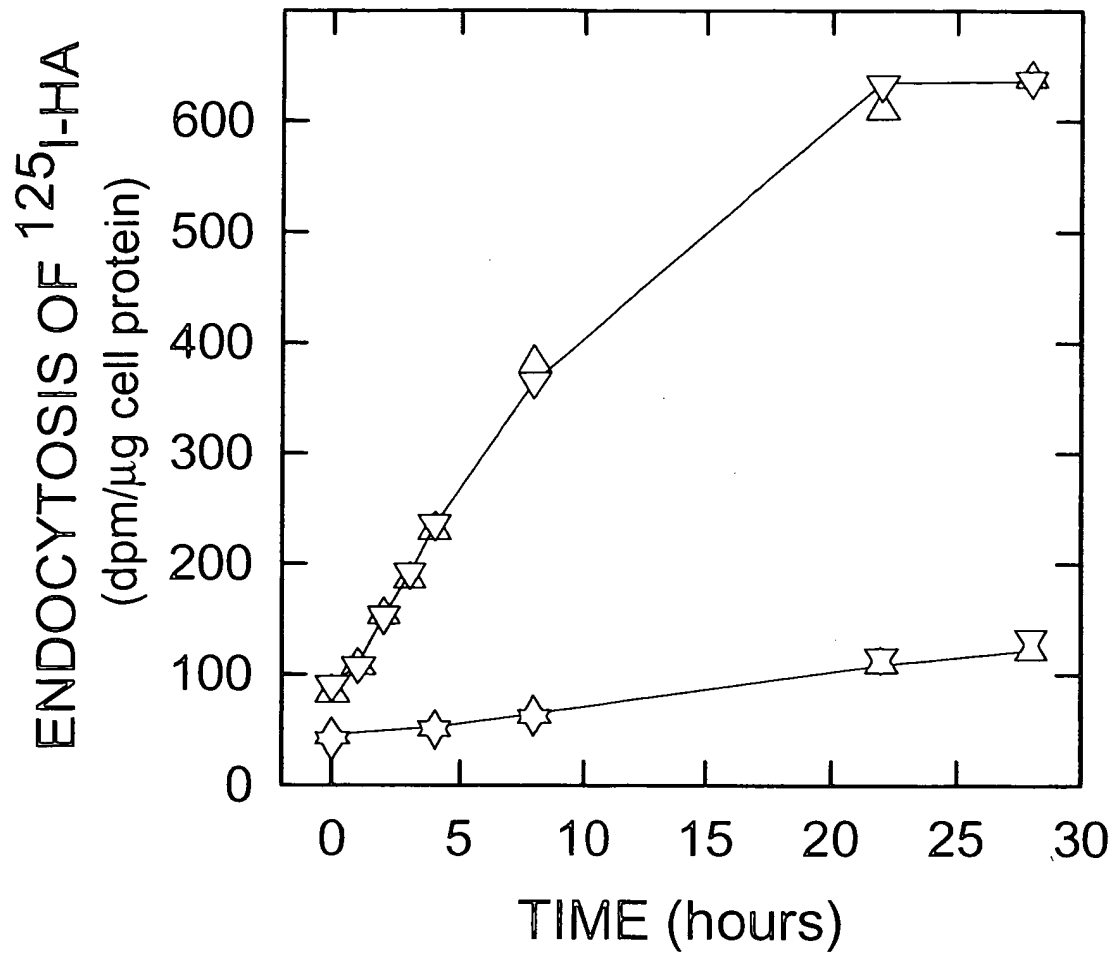


Figure 27B

Degradation of internalized HA by transfected SK-Hep1 cell lines expressing the 175-kDa HARE

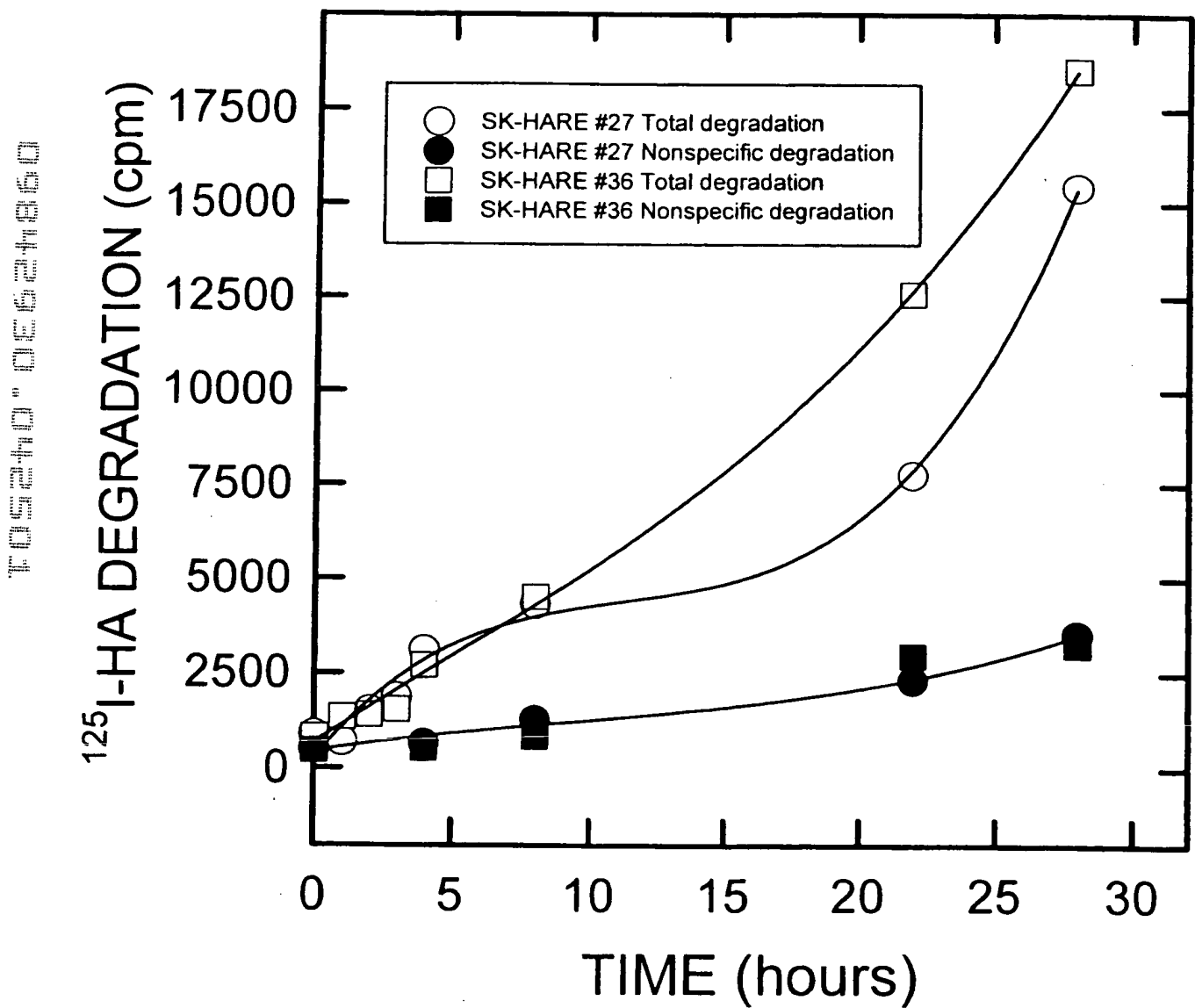


Figure 27C

Hyperosmolarity inhibits HA endocytosis mediated by HARE in transfected SK-Hep1 cells

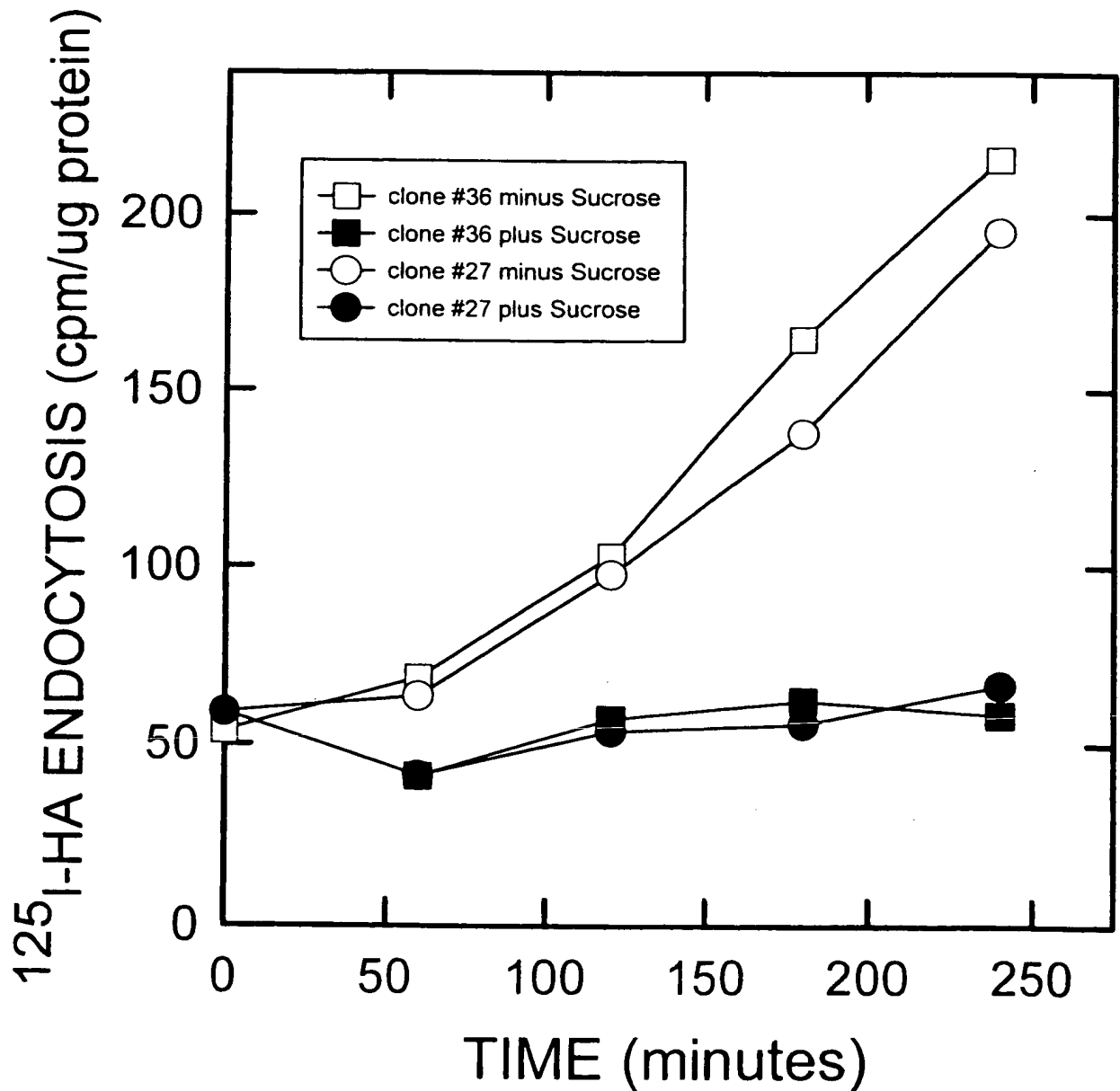


Figure 27D

**Specific monoclonal antibodies against HARE
inhibit HA endocytosis in SK-Hep1
transfectants expressing the 175-kDa HARE**

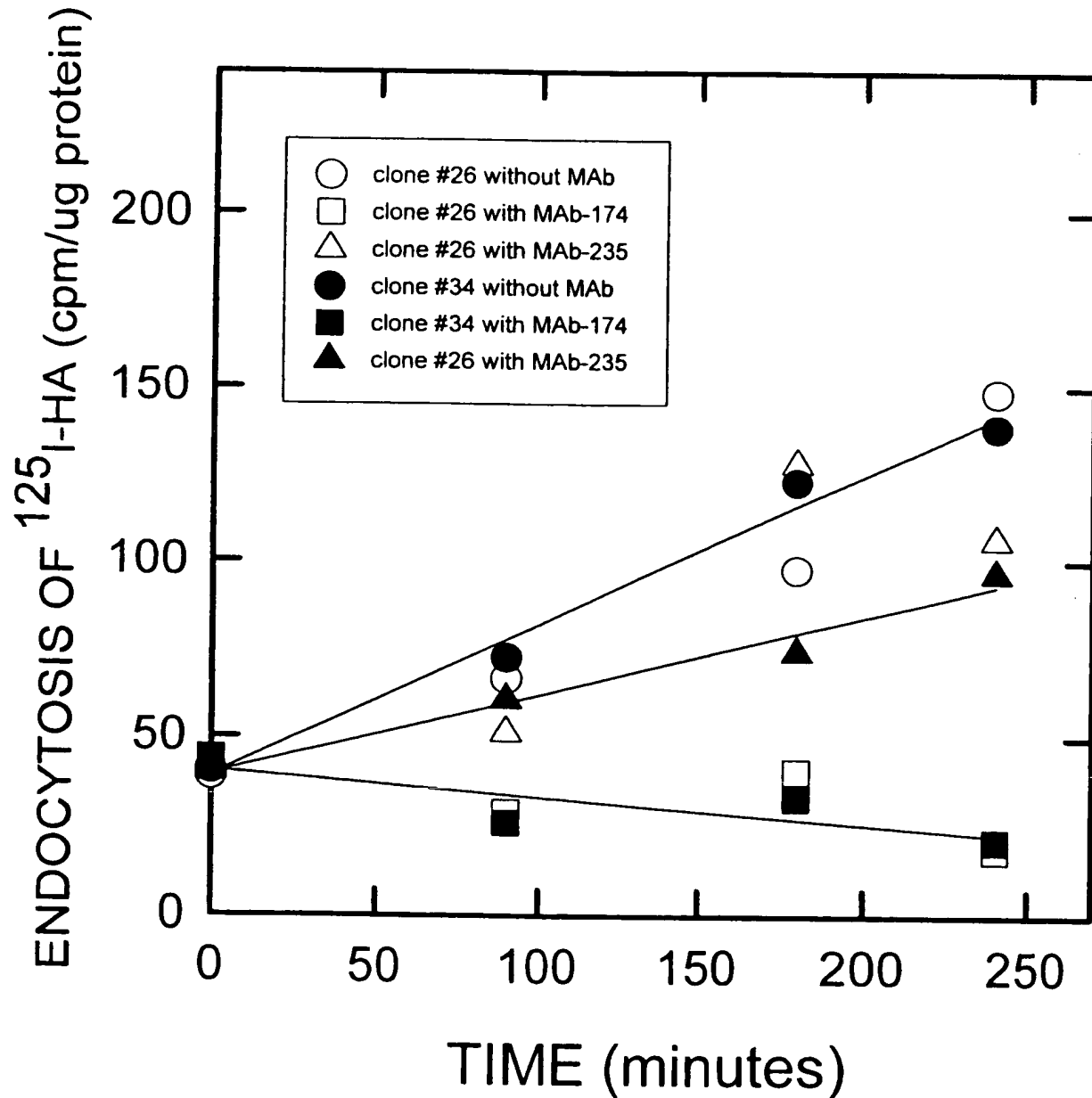


Figure 28

175SHARE	1	-----SLPS	LLTRLEQMPD	YSIPRGYI IH	YNLASAIESA	DAYTVFVFN	EAIENYIREK	KATSLKED IL	RYHVVLGKEL	LKNDLHNGMH	RETM LGFSYL
CAB61827	1111	LHLISQVLLP	PRGDVPGGQG	LLQQLDLVPA	FSLPRELLHG	HGLVPOIEAA	TATYTFVPTN	RSLEA ---QG	NSSHLDADTV	RHHVVLGEAL	SMETLRKGH
BAA13377	754	LHLISQVLLP	PRGDVPGGQG	LLQQLDLV-A	FSLPRELLHG	HGLVPOIEAA	TATYTFVPTN	RSLEA ---QG	NSSHLDADTV	RHHVVLGEAL	SMETLRKGH
175SHARE	95	LAFFLRNDQL	YVNEAP INYT	NVATDKGVH	GLEKVLIEQK	NRQDNDNTH	VRECGKQSQ	QAFPLETKP	LETRK -CIV	SIYFMGRSV	FICQPOQVR
CAB61827	1218	IVFYNHSSQP	EVNHVPLEGP	MLEAPGRSLI	GLSGVLTVGS	SRQLHSHAEE	LREKQVNTTR	RFRCTQGFOL	QDTPRKSCVY	RSGPSFSR--	---GGSYDIAK
BAA13377	861	IVFYNHSSQP	EVNHVPLEGP	MLEAPGRSLI	GLSGVLTVGS	SRQLHSHAEE	LREKQVNTTR	RFRCTQGFOL	QDTPRKSCVY	RSGPSFSR--	---GGSYDIAK
175SHARE	204	SLAHNAK PAP	GEVK-MQALG	TASVMDGVNG	TGTPOEGLGF	NGTACETETE	GKYGIHCDQA	CSQVHGRQSQ	GPLGDGSCDC	DVGHGRGVKD	MEITTDNNG
BAB15793	1	-----	-----W	HLFGWS--DG	TGVPEGEGGF	SGTACETETE	GKYGIHCDQA	CSQVHGRQSQ	GPLGDGSCDC	DVGHGRGVKD	NATTTEDNNG
CAB61358	1	-----	-----W	HLFGWS--DG	TGVPEGEGGF	SGTACETETE	GKYGIHCDQA	CSQVHGRQSQ	GPLGDGSCDC	DVGHGRGVKD	NATTTEDNNG
CAB61827	1224	FFGTLCPECP	GGLGGVQS-G	HGCCQDRFLG	SGEHCHEGPF	HGTACEVDEL	GRYGPNTGV	CHQAHGLQOE	GLOGDGSCVC	NVGHQGLRCD	QKITSPOQPR
BAA13377	967	FFGTLCPECP	GGLGGVQS-G	HGCCQDRFLG	SGEHCHEGPF	HGTACEVDEL	GRYGPNTGV	CHQAHGLQOE	GLOGDGSCVC	NVGHQGLRCD	QKITSPOQPR
175SHARE	313	DPDGKASCKC	AAGFRGNGTV	CTAINACETS	NGGCSKADK	KRTTPGNRVG	VCKAGYTDGD	IVCLEINPCL	ENHGGCDRNA	ECTQTGPNQA	VENCLPKYTG
BAB15793	90	NSDGTASCKC	AAGFGQNGTI	CTAINACETS	NGGCSKADK	KRTTPGNRVG	TCKAGYTDGD	IVCLEINPCL	ENHGGCDRNA	ECTQTGPNQA	ACNCLPAYTG
CAB61358	3	EAVGTASCKC	AAGFGQNGTI	CTAINACETS	NGGCSKADK	KRTTPGNRVG	TCKAGYTDGD	IVCLEINPCL	ENHGGCDRNA	ECTQTGPNQA	ACNCLPAYTG
CAB61827	1433	DSAGASTQAC	AAGYSGNGIF	CSEVDPCAAG	HGGCSPHANC	TKVAPQQRIC	TQGDYMGDGG	ELCQBEINSCL	IHHGGCH IHA	ECIPTGQQV	SQSCREGYSG
BAA13377	1076	DSAGASTQAC	AAGYSGNGIF	CSEVDPCAAG	HGGCSPHANC	TKVAPQQRIC	TQGDYMGDGG	ELCQBEINSCL	IHHGGCH IHA	ECIPTGQQV	SQSCREGYSG
175SHARE	422	VCLTNNGGCS	PFAPCNYTEQ	DQRICTCKPD	Y-TGDGIVCR	GSIIYELPKN	PSTSQYFPQL	QEHAVRELAG	PGPFTVFAP-	--LSSSFNHE	PRIKDWDQGG
BAB15793	199	VCLTNNGGCS	PFAPCNYTEQ	VERTCTCKPN	Y-IGDFTCR	GSIIYELPKN	PSTSQYFPQL	QEHAVRELAG	PGPFTVFAP-	--LSSSFNHE	PRIKDWDQGG
CAB61358	112	VCLTNNGGCS	PFAPCNYTEQ	VERTCTCKPN	Y-IGDFTCR	GSIIYELPKN	PSTSQYFPQL	QEHAVRELAG	PGPFTVFAP-	--LSSSFNHE	PRIKDWDQGG
AAF82398	1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
CAB61827	1543	PQSKNNGGCS	PYATCKSTGD	QORTCTCTDA	HTVGDGLTFR	ARVGLLELRD	KHAS--FFSL	RLLEYKELKG	DGPFTTIFVPH	ADLMSNLSQD	ELARIRAHQK
BAA13377	1186	PQSKNNGGCS	PYATCKSTGD	QORTCTCTDA	HTVGDGLTFR	ARVGLLELRD	KHAS--FFSL	RLLEYKELKG	DGPFTTIFVPH	ADLMSNLSQD	ELARIRAHQK
175SHARE	528	VGCQQLLLEN	LKVTTSATTL	QGEVVISVS	QDTVFINNEA	KVLSSDIIST	NGVIHV IDKL	LSPKNLLITP	KDALGRVLQN	LTTVAANHYG	TKFSKLQDS
BAB15793	305	VACHQLLLEN	LKLISNATSL	QGEVVISVS	QSTVYINNKA	KI TSSDIIST	NGVIHV IDKL	LSPKNLLITP	KDMSGRILQN	LTTLATNNGY	I KFSNLQDS
CAB61358	218	VACHQLLLEN	LKLISNATSL	QGEVVISVS	QSTVYINNKA	KI TSSDIIST	NGVIHV IDKL	LSPKNLLITP	KDMSGRILQN	LTTLATNNGY	I KFSNLQDS
AAF82398	10	VACHQLLLEN	LKLISNATSL	QGEVVISVS	QSTVYINNKA	KI TSSDIIST	NGVIHV IDKL	LSPKNLLITP	KDMSGRILQN	LTTLATNNGY	I KFSNLQDS
CAB61827	1648	VGCRRRLSED	LLEQGYATAL	SGHPLRFSE	BGSIIYNDFA	RUVSSDHEAV	NGILHF IDRV	LLPPEALHWE	PDDAPIPRRN	VTAAAGQFGY	KIFSGLLKVA
BAA13377	1291	VGCRRRLSED	LLEQGYATAL	SGHPLRFSE	BGSIIYNDFA	RUVSSDHEAV	NGILHF IDRV	LLPPEALHWE	PDDAPIPRRN	VTAAAGQFGY	KIFSGLLKVA
175SHARE	638	HTPVTVFWPT	DKALEALPPE	QODFLFNQDN	KDKLKSYLEK	HVIRDSKALA	SDLPRASWK	TLQGSSELSV	CGTGSDIGEL	FLNBQMCRFI	HGRLLFDVGV
BAB15793	415	HTPVTVFWPT	DQALHALPAE	QODFLFNQDN	KDKLKSYLEK	HVIRDAK VLA	VDLPTSTAWK	TLQGSSELSV	CGAGRDIGDL	FLNGQTCRIV	QRELLFDLGV
CAB61358	328	HTPVTVFWPT	DQALHALPAE	QODFLFNQDN	KDKLKSYLEK	HVIRDAK VLA	VDLPTSTAWK	TLQGSSELSV	CGAGRDIGDL	FLNGQTCRIV	QRELLFDLGV
AAF82398	120	HTPVTVFWPT	DQALHALPAE	QODFLFNQDN	KDKLKSYLEK	HVIRDAK VLA	VDLPTSTAWK	TLQGSSELSV	CGAGRDIGDL	FLNGQTCRIV	QRELLFDLGV
CAB61827	1758	HRPFTMLWPT	DAAFRALPFD	RQAWLYHEDH	RDKLAAILRG	HMRINVEALA	SDLPNLGLPLR	TMHGTPISFS	CSRTRP-GEL	MVGEDDARIV	QRLHPPBGGL
BAA13377	1401	HRPFTMLWPT	DAAFRALPFD	RQAWLYHEDH	RDKLAAILRG	HMRINVEALA	SDLPNLGLPLR	TMHGTPISFS	CSRTRP-GEL	MVGEDDARIV	QRLHPPBGGL
175SHARE	748	PTLGGRCDTF	TTFDIP-GE	GSQIFTPKCF	LKSKPKGVKQ	KC--LY----	N-LPF	K-----	---RNLE-GC	QNLCTVVIQT	PROCKGYFGR
BAB15793	425	PTLGGRCDTF	TTFDAS-GE	GSQVNTSPCF	RWSKPKGVKQ	KC--LY----	N-LPF	K-----	---RNLE-GC	QNLCTVVIQT	PROCKGYFGR
CAB61358	538	PTLGGRCDTF	TTFDAS-GE	GSQVNTSPCF	RWSKPKGVKQ	KC--LY----	N-LPF	K-----	---RNLE-GC	QNLCTVVIQT	PROCKGYFGR
AAF82398	230	PTLGGRCDTF	TTFDAS-GE	GSQVNTSPCF	RWSKPKGVKQ	KC--LY----	N-LPF	K-----	---RNLE-GC	QNLCTVVIQT	PROCKGYFGR
CAB61827	1867	PGLGARCDHF	ETRLPRLNTC	SICGLEPPCF	BGSQBGSGPE	ACWRFPYKFW	TSPPHLSGL	RSVWVHPSLW	GRPGGLGRGC	HRNCTVTTWK	SCQCPGHYGS
BAA13377	1510	PGLGARCDHF	ETRLPRLNTC	SICGLEPPCF	BGSQBGSGPE	ACWRFPYKFW	TSPPHLSGL	RSVWVHPSLW	GRPGGLGRGC	HRNCTVTTWK	SCQCPGHYGS
175SHARE	833	TPCNRNRCGR	DLYTPMGQCL	QHTGFNGTAC	ELCWHGRFGP	DCQPRSCSEH	GCQDEGITS	GCQCLCEGT	AASCDTPAV	PAVCTPPCSA	HATCKENNTC
BAB15793	609	APCNRNRCGR	DOYSATGECK	QHTGFNGTAC	ELCWHGRFGP	DCQPRSCSEH	GCQDEGITS	GCQCLCEGT	GPSCDTQAVL	PAVCTPPCSA	HATCKENNTC
CAB61358	522	APCNRNRCGR	DOYSATGECK	QHTGFNGTAC	ELCWHGRFGP	DCQPRSCSEH	GCQDEGITS	GCQCLCEGT	GPSCDTQAVL	PAVCTPPCSA	HATCKENNTC
AAF82398	314	APCNRNRCGR	DOYSATGECK	QHTGFNGTAC	ELCWHGRFGP	DCQPRSCSEH	GCQDEGITS	GCQCLCEGT	GPSCDTQAVL	PAVCTPPCSA	HATCKENNTC
CAB61827	1977	SPQSDRGVCM	DCMSGSGQCL	CRSGFAGTAC	ELCAGAGAGP	HCQACRCIVH	GRCDGLOGS	GSQFCEDEGT	GPSCDTQAVL	PAVCTPPCSA	HATCKENNTC
BAA13377	1620	SPQSDRGVCM	DCMSGSGQCL	CRSGFAGTAC	ELCAGAGAGP	HCQACRCIVH	GRCDGLOGS	GSQFCEDEGT	GPSCDTQAVL	PAVCTPPCSA	HATCKENNTC
175SHARE	943	ITCTVVDPRK	QNNGGCAKVA	RCSQKGTQVS	CSCQKGYKGD	GHSCITEIDPC	ADGLNGGCH	HATCKMTGPG	KHKCEKSHY	VGDGLNCEP	EQLPIDRCLQ
BAB15793	719	ITCTVVDPRK	QNNGGCAKVA	RCSQKGTQVS	CSCQKGYKGD	GHSCITEIDPC	ADGLNGGCH	HATCKMTGPG	KHKCEKSHY	VGDGLNCEP	EQLPIDRCLQ
CAB61358	632	ITCTVVDPRK	QNNGGCAKVA	RCSQKGTQVS	CSCQKGYKGD	GHSCITEIDPC	ADGLNGGCH	HATCKMTGPG	KHKCEKSHY	VGDGLNCEP	EQLPIDRCLQ
AAF82398	424	ITCTVVDPRK	QNNGGCAKVA	RCSQKGTQVS	CSCQKGYKGD	GHSCITEIDPC	ADGLNGGCH	HATCKMTGPG	KHKCEKSHY	VGDGLNCEP	EQLPIDRCLQ
CAB61827	2087	RVCITVADLCQ	DGHGCGSEHA	NCSQVGTMTV	GTCLPDPYEG	GWSCRARNPC	TDGHRRGQSE	HANCLSTGLN	TRRCBCHAGY	VGDGLNCEP	EQLPIDRCLQ
BAA13377	1730	RVCITVADLCQ	DGHGCGSEHA	NCSQVGTMTV	GTCLPDPYEG	GWSCRARNPC	TDGHRRGQSE	HANCLSTGLN	TRRCBCHAGY	VGDGLNCEP	EQLPIDRCLQ
175SHARE	1052	CADLYFQDIT	VGVPFLRSPL	QGYKLTDPKA	KEACANEAAAT	MATYNQLSYA	QKAKYHLCSA	GWLESGRVAY	PTAFASQNCG	SGVVGIVDYG	PRPNKSEMD
BAB15793	828	CVDLHFQDIT	VGVPFLRSPL	QGYKLTDPKA	KEACANEAAAT	MATYNQLSYA	QKAKYHLCSA	GWLESGRVAY	PTAFASQNCG	SGVVGIVDYG	PRPNKSEMD
CAB61358	741	CVDLHFQDIT	VGVPFLRSPL	QGYKLTDPKA	KEACANEAAAT	MATYNQLSYA	QKAKYHLCSA	GWLESGRVAY	PTAFASQNCG	SGVVGIVDYG	PRPNKSEMD
AAF82398	533	CVDLHFQDIT	VGVPFLRSPL	QGYKLTDPKA	KEACANEAAAT	MATYNQLSYA	QKAKYHLCSA	GWLESGRVAY	PTAFASQNCG	SGVVGIVDYG	PRPNKSEMD
CAB61827	2197	CTDQHFQEK	AGVPHLOATS	GPYGLNFPSEA	EAAQEAQAGAV	LA SFPQLSAA	QQLGPHLQML	GWLANGSTAH	PVVFPVADCG	NGRVGIVSLG	ARKNLSERHD
BAA13377	1840	CTDQHFQEK	AGVPHLOATS	GPYGLNFPSEA	EAAQEAQAGAV	LA SFPQLSAA	QQLGPHLQML	GWLANGSTAH	PVVFPVADCG	NGRVGIVSLG	ARKNLSERHD
175SHARE	1162	CTCKAGYVGD	GFS--BSGNLL	QVLMSPFSLT	NFLTEVLAYS	KSSARQAFL	KHLTDLISRG	TLFVPQNSGL	PGNKSLSGRD	IEHHLTNVNV	SFYNDLVNGT
BAB15793	938	CTCKAGYVGD	GFS--BSGNLL	QVLMSPFSLT	NFLTEVLAYS	KSSARQAFL	KHLTDLISRG	TLFVPQNSGL	PGNKSLSGRD	IEHHLTNVNV	SFYNDLVNGT
CAB61358	849	CTCKAGYVGD	GFS--BSGNLL	QVLMSPFSLT	NFLTEVLAYS	KSSARQAFL	KHLTDLISRG	TLFVPQNSGL	PGNKSLSGRD	IEHHLTNVNV	SFYNDLVNGT
AAF82398	643	CTCKAGYVGD	GFS--BSGNLL	QVLMSPFSLT	NFLTEVLAYS	KSSARQAFL	KHLTDLISRG	TLFVPQNSGL	PGNKSLSGRD	IEHHLTNVNV	SFYNDLVNGT
CAB61827	2307	CTCKAGYVGD	GFS--BSGNLL	QVLMSPFSLT	NFLTEVLAYS	KSSARQAFL	KHLTDLISRG	TLFVPQNSGL	PGNKSLSGRD	IEHHLTNVNV	SFYNDLVNGT
BAA13377	1950	CTCKAGYVGD	GFS--BSGNLL	QVLMSPFSLT	NFLTEVLAYS	KSSARQAFL	KHLTDLISRG	TLFVPQNSGL	PGNKSLSGRD	IEHHLTNVNV	SFYNDLVNGT
175SHARE	1271	LITAS--QD	QLHQ-ETRFV	DGRSILQWDI	IAANGILHII	SEPLRAPPTA	ATA---AHSG	LGTFICFAVV	LVTGAIA--L	AAYSYFRIRK	RTTG--FQPF
BAB15793	1047	LITAS--QD	PLQPTETRFV	DGRSILQWDI	PASNGIIHVI	SRPLKAPPAP	VTL---THIG	LGAGIFFAII	LVTGAIA--L	AAYSYFRINR	RTTG--FQPF
CAB61358	924	LITAS--QD	PLQPTETRFV	DGRSILQWDI	PASNGIIHVI	SRPLKAPPAP	VTL---THIG	LGAGIFFAII	LVTGAIA--L	AAYSYFRINR	RTTG--FQPF
AAF82398	752	LITAS--QD	PLQPTETRFV	DGRSILQWDI	PASNGIIHVI	SRPLKAPPAP	VTL---THIG	LGAGIFFAII	LVTGAIA--L	AAYSYFRINR	RTTG--FQPF
CAB61827	2416	II SDAGPDNS	SWAPVAPGTV	VVSRIIVWDI	MAFNGIIHAL	ASPLLAPOP	QAVLAPEAPP	VAAGV--GAV	LAAGALLGLV	AGATVLRARG	KPMGPGFSAP
BAA13377	2059	II SDAGPDNS	SWAPVAPGTV	VVSRIIVWDI	MAFNGIIHAL	ASPLLAPOP	QAVLAPEAPP	VAAGV--GAV	LAAGALLGLV	AGATVLRARG	KPMGPGFSAP
175SHARE	1170	LASSSP-RIS	QTLCMRQRR	HPQSPPVTPS	QTLNRIWRT	ATLWGHCQPD	MRSQQATVTV	VPR	-----	-----	-----
BAB15793	1347	LKGQOPENIS	NPLY-ESTTS	APPEPSYDPP	TDS EER----	-----	-----	-----	-----	-----	-----
CAB61358	1024	LKGQOPENIS	NPLY-ESTTS	APPEPSYDPP	TDS EER----	-----	-----	-----	-----	-----	-----
AAF82398	852	LKGQOPENIS	NPLY-ESTTS	APPEPSYDPP	TDS EER----	-----	-----	-----	-----	-----	-----
CAB61827	2524	SPWQ-EGTN	PTLVSV PNPV	FGSDTCEPFP	DD-----	-----	-----	-----	-----	-----	-----
BAA13377	2166	SPWQ-EGTN	PTLVSV PNPV	FGSDTCEPFP	DD-----	-----	-----	-----	-----	-----	-----

Figure 29

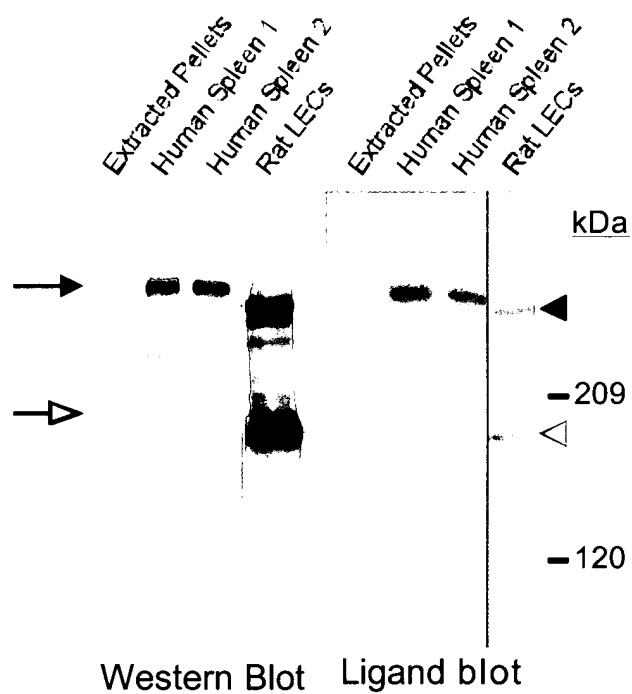


Figure 3

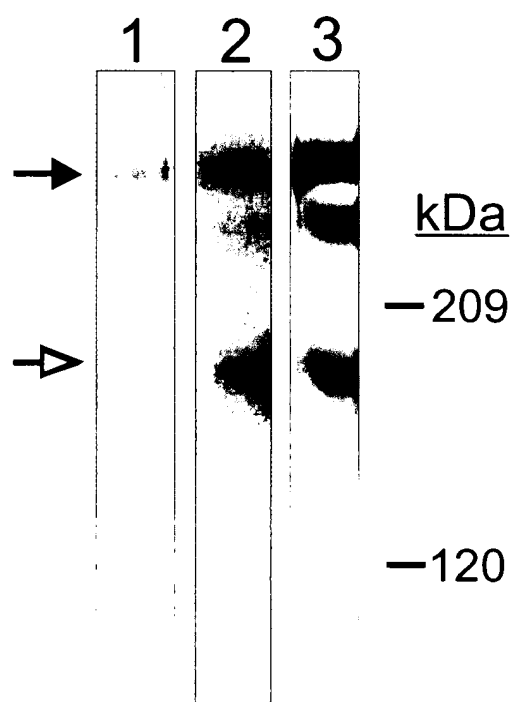


Figure 31

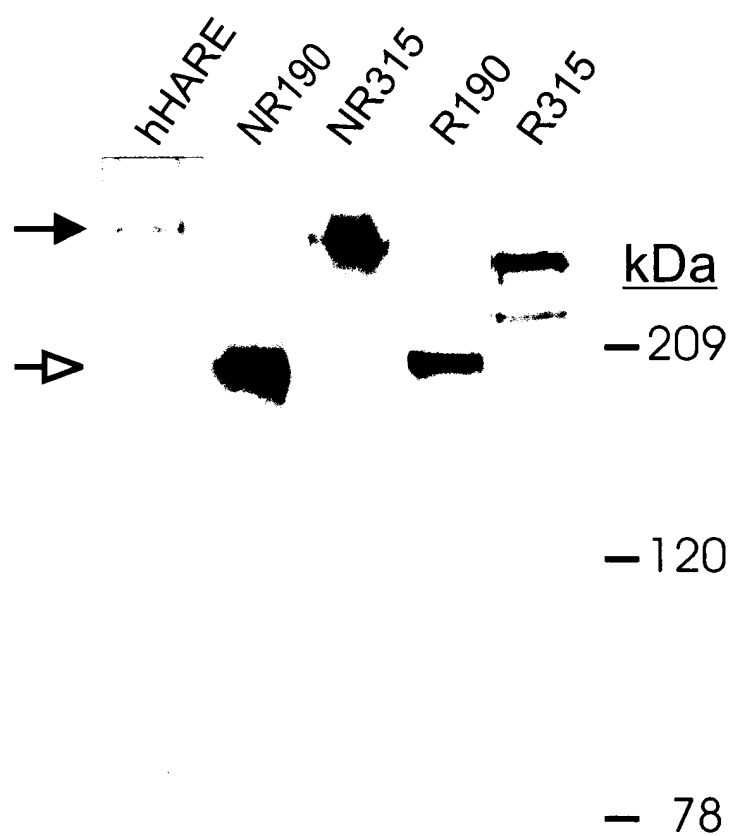
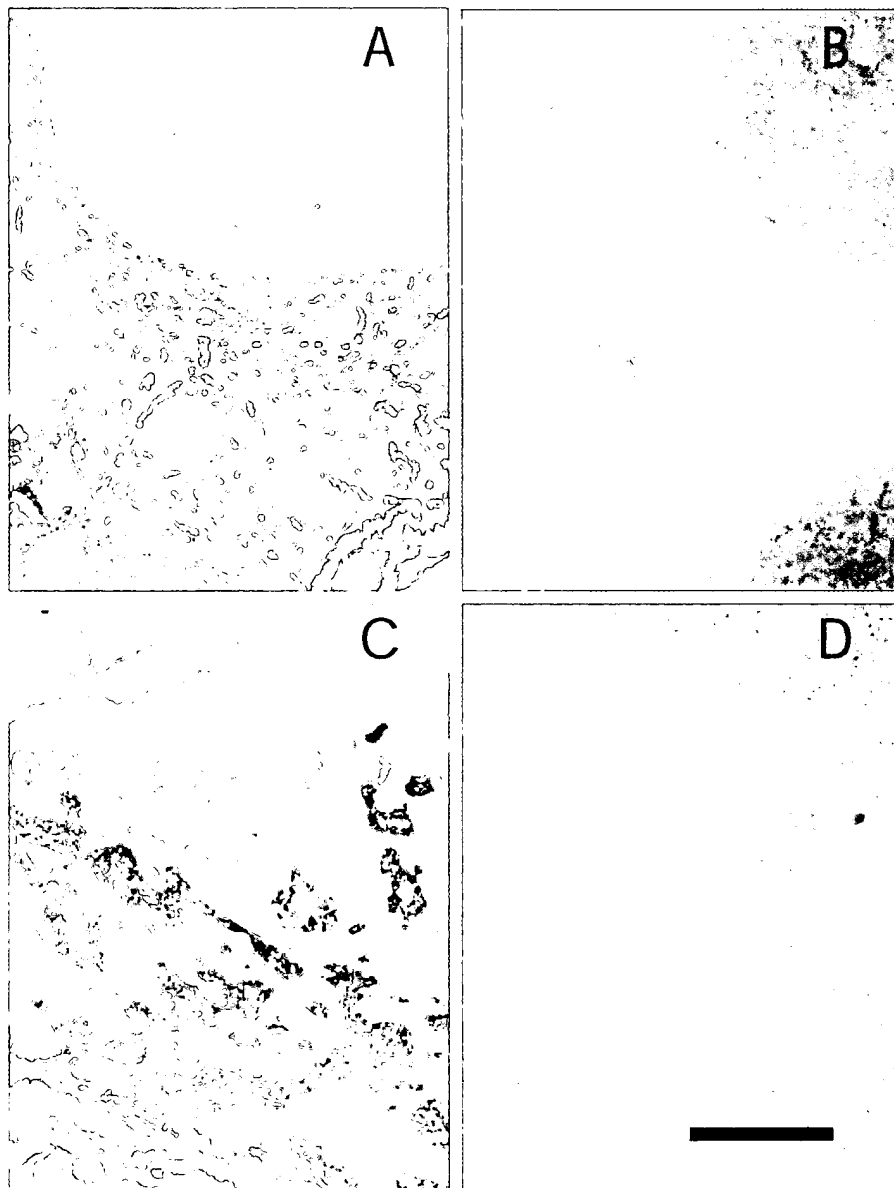


Figure 3 2



[illegible]

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I Q Y N L A N A I E A A D A Y T V F A P N N N A I E N Y I C A G G R E K K K V L S L E E D

121 GTCTCCGTTTCATGTGGTCTGGAGGAAAACCTGTAAGAATGACCTGACACATGGCATGCTGAGACCATGTCTGGGTTCTCTTATCTTCTTAGCTTCTTCTCCATAATGAC
41 V C C R Y H V V L E E K L L K N D L H N G M G R C T G T G L F S Y F L S F F L H N D

241 CAGCTCTATGTAATAGGAGCTCCAATAAACTACCAAATGTAGCCACTGATAAGGAAATGTATGATCCATGGCTTGGGAAAAATCTCTGGAAATTCAGAAACAGATGTGATAATAATGACACT
81 Q L Y V N N E A P I N Y T N V A T D K G V I H G L G K V L E I Q K N N R C D N N D T

361 ACTATTATACGAGAAGATGTAGAACCTCTCCACAGCTGACCTGCCATTCGGAATCTCTAGTAAATGAGAAGGAGGATGCATCTATACCTCTTATCTGAGGAAGACGA
121 T I I R G R C R T C S S E L T C P F G T K S L G N E K R R C I Y T S Y F M G R R

481 ACCTGTTTTATTGGGTCGCCAACAATGTGTAGAACCGGTATTACGAGAAATGCTGTCCGGCTCTTTGGCCCCAATGCCAGCCCTGTCTCAGGGAATGCCAGAAATCTGTGCTTT
161 T L F I G C Q K C V R T V I T R E C C A G F F G P Q C Q P C P G N A Q N V C T C P

601 GGTAATGGCATCTGTTTGGATGGAGTGAATGGCAAGGTGTGTGTGTGTGTGGGAGGCTTCAGCGGCACAGCCTGCGAGACCTGCACCGAGGCGAATCAGGACCTCACTGTGACCAA
201 G N G I C L D G V N G T G V C E C G E G F S G T A C E T C T E G E K Y G I H C D Q

721 GCATGTTCTTGTGTGGAGATGCAACCAAGACCCCTGGGAGATGGCTCTGTGACTGTGATGTGGCTGGCGAGGATGCATTTGACAAATGCAACCAAGGAGCAATGCAAT
241 A C S C V H G R C N Q G P L G D G S C D C D V G W R G V H C D N A T T E D N C

841 GGGACATGCCATACCAGCGCAACTGCTCACCAACTCAGATGGTACAGCTTCATGCAAGTGTGCAGCAGGATTCCAAGGAAACGGGACCATCTGCACAGCAATCAATGCCTGTGAGATC
961 G T C H T S A N C S S D G T A S C K C A A G F Q G N G T I C T A I N A C E I

981 AGCAATGGAGTTGCTCTGCCAAGGCTGACTGTAAGAGAACCACCCAGGAAGCGAGTGTGCACGTGCAAGAGCAGGCTACACGGGTGTGGCATTGTGCTGGAAATCAACCCGTGT
321 S N G G C S A K A D C K R T T P G R V C T K A G Y T G D G I V C L E I N P C

1081 TTGGAGAACCATGGTGTGTGACAAAGATGGGAGTGCACACAGACGCCAACCCAGGCTGCCTGTAACCTTTTGGCAGCATACATGGAGATGGAAGGCTGTGCACACTCATCAAT
361 L E N H G G C D K N A E C T Q T G P N Q A A C N C L P A Y T G D G K V C T T L I N

1201 GTCTGCTTAATAAAATGGCGGCTGTAGTGAATTTGCCATGTGCAACCAACATGGGCAAGTAGAAGAGCTTTGACTTGCAGCCAACTACATTGGAGATGGATTACTTCCGCGGG
401 V C L T K N G G C S E F A I C N H T G Q V E R T C T C K K P N Y I G D G P T C R G

1321 AGCATTTATCAGGAGCTTCCCAGAACCCGAAACTTCCAGTATTTCTCCAGTTGCAGGAGCAATTCGTGAAGATCTGGTGGCCCGCCGCCCTTCACTGTTTTCGACCTTTATCT
441 S I Y Q E L P K N P K T S Q Y F P O L Q E H P V K D L V G P G P F T V F A P L S

1441 GCAGCCTTTGATGAGGAAGCTCGGTTAAAGACTGGGACAAATACGGTTTATGGCCAGGCTTCTGGCTACCATGTGGTGCCTGCCACAGCTGCTTCTGGAAACCTGAAATKLTATC
481 A A F D E E A R V K D W D K I Y G L M P Q V L R Y H V V A C H Q L L L E N L K L I

1561 TCAAATGCTACTTCCCTCAAAGAGGCCAATGATCATCTCCGCTCTCAGACACGGTGTATATAAACAATAAGGCAAGATCATATCCAGTGATCATCAGTACTAATGGGATGTT
521 S N A T S L Q G E P I V I S V S Q S T V I N N K A K I I S S D I I S T N G I V

1681 CATATCATAGACAAATGCTATCTCCCAAAATTTGCTTATCACTCCCAAGACAACCTCTGGAAGAAATCTGC AAAATCTTACGACTTTGGCAACAAACATGGGTACATCAAAATTTAGC
561 H I I D K L S P K N L L I T P K D N S G R I L Q N L T T L A T N N G Y I K F S

1801 AACTTAATACAGGACTCAGTTTGTGAGTGTATCCGATPCCIHTFPVTFLFWPTDQALHALPAEAGQGADPF
601 N L I Q D S G L L S V I T C C G A C C C A G C A C T C T T C T G C C C A C C G A A G C C T C C A T G C C T A C T G T A A C C A G G A C T T C

1921 CTGTTCACCAAGACCAAGGACAAGCTGAAGGAAATTTGAATCTTCATGTATGACGATGCAAGGTTTGTAGCTGTGGATCTTCCACATCCACTGCCTGGAAGACCTGCAAGGT
641 L F N Q D N K D K L K E Y L K I F H V I R D A K V L A V D L P T S T A W K T L Q G I

2041 TCAGAGCTGAGTGTGAATGTGAGCTGGCAGGACATCGTGACCTCTTCTGAATGGCAACCTGCAGAAATTTGTCAGCGGAGCTTGTGTGACCTGGGTGTGGCTACGGCT
681 S E L S V K I C G A G R D I G D L F L N G O T C R I V Q R E L L F D L G V A Y G I

2161 GACTGCTGCTGATTGATCCCACTGGGCGCGCTGTGACACCTTTACTATTTTCATGCTCGGGGAGTGTGGAGCTGTGTCAATCTCCAGCTGCCAAGGCTGAGTAAACCA
721 D C L L I D P T L G G R C D T F T T F D A S G E C G S C V N T P S C P R W S K P

2281 AAGGTGTGAAGCAGAAGTGTCTTACAACCTGCCCTTCAAGAGGAACCTGGAAGGCTGCCGGGAGCGGTGCAGCCTGGTGATACAGATCCCAAGGTGTGCAAGGCTCTCGGGCA
761 K G V K Q K C L Y N L P F K R N L E G C R E R E C S L V I Q I P R C C K I G Y F G R I

2401 GACTGTCCAGCTGCCCTGGAAGCAGATGCCCGCTGAATAACCCGGGTGTCTGCTGTATCAGTACTCGGCACCGGAGAGTGTAATGCAACACCGGCTCAATGGGACCGCGTGT
801 D C Q A C P G G P D A P C N N R G V C L D Q Y S A C G E C K C N T G F N G T A C T

2521 GAGATGTGCTGGCGGGAGATTTGGGCTGATTTGTCTGCCCTGTGGCTGCTCAGACCAAGCAGTGCATGATGGCATCACGGGCTCCGGGAGTGCCTCTGTGAAACGGGTTGGACA
841 E M C W P G R F G P D C L P C G C S D H G C C D D G I A T G S G Q C L C E T G W T

2641 GGCCCTCTGTGATCACTCAGGAGTTTGGCTGCACTGTGTACGCTCTTGTCTGATGCACTGTGAAGGAGAACACAGCTGTGAGTGTAACTGATTAAGGTGACGGA
881 G P S C D T Q A V L P A V C A C T G C T A H A T C K E N N N T C E C N L D Y E G D G

2761 ATCACTGCACAGTTGTGGATTTCTGCAACAGGACAACCGGGGCTGTGCAAGAGTGGCCAGATGCTCCAGAAAGGCGCAAGAGGCTCTCTGAGCTGCCAGAGGATGAAAGGGG
921 I T C T V V D F C Q D N G G C A K A V A R C S Q K G T K V S C S C Q K G G A Y K G D

2881 GGGCAGAGCTGCACAGAGATAGACCCCTGTGCAGACGGCCTTAACCGAGGGTGTACAGCAGCCACCTGTAAGATGACAGGCGCGGCAAGCACAAGTGTGATTAAGTCACTAT
961 G H S C T E I D P C A D G L N N G G C H E H A T C K M T G P G K H K C E C K S H Y

3001 GTCCGAGATGGGCTGAATCTGTAGCCGAGCAGTGCCTTACAGCGCTGTCTACAGGACATGGGAGTGGCATGCAGACGCAAAATGTGTGACCTTCCAGGATACCACTGTT
1001 V G D G L N C E P E Q L P I D R C L Q D N G C H A D A K C V D L H F Q D T T V

3121 GGGGTGTTCCATCTACGCTCCCACTGGGCGAGTATAAGCTGACCTTTGACAAABCCAGABAGGCTGTGCCAACGAAGCTGCGACCATGGCAACCTACAACAGCTCTCTATGCCAG
1041 G V F H L R S P L G Q Y K L T F D K A R I E A C A N E A A T M A T Y N Q L S Y A Q

3241 AAGGCCAAGTACACCTGTGCTCAGCAGCTGGCTGGAGACCGGCGGGTGTGCTTACCCACAGCCTTCGCTCCAGAACTGTGGTGTGGTGTGGGATGTGGATATGGACCT
1081 K A K Y H L C S A G W L E T G R V A Y P T A F A S Q N C G S G V V G I V D Y G P

3361 AGACCAACAAGAGTGAATGTGGGATGTTCTCTGCTATCGGATGAAGATGTGAATCTGACCTGCAAGGTGGGCTATGTGGAGATGGCTTCTCATGAGTGGGAACCTGTGCAAGT
1121 R P N K S E M W D V C F Y R M K D V N C T C K V G Y V G D G F S C S G N L L Q V

3481 CTGATGCTCTTCCCTCACTCACAACCTTCTGAGGAAAGTGTGGCCTATTCCAACAGCTCAGCTGAGGCGGTGCAATTCTAGAACACTGACTGACTGTCCATCGCGGACCTC
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3601 TTGTGCCACAGACAGTGGTGGGGGCAATGAGACCTTGTCTGGGCGGACATCAGACCAACCTCGCAATGTTCAGCATGTTTCTCAATGACCTTGTCAATGGACCAACCTG
1201 F V P Q N S G S L G E N E T L S G R D I E H H L A N V S M F F Y N D L V N G T T L

3721 CAACGAGGCTGGGAAGCAAGCTGCTCATCTGCTCAGCAGCAGGACCCACTCCAACCGAGCGAGACAGGTTTGTGTGGAAGAGCCATTCTGCAGTGGGACATCTTGGCTCAATGGG
1241 Q T R L G S K L L I T A S Q D P L Q P T E T R F V D G R A I L Q W D I F A S N G

3841 ATCATGTATGCTTCCAGGCTTTAAAGACACCCCTGCCCGGCTGACCTTGACCACTGGCTTGGAGAGCGGGATCTCTTGGCATCACTCTGGTGAAGCTGGGCTGTGCTG
1281 I H V I S R P L K A P P A P V T L T H T G L G A G A G I F F A I L V T G A V A L

3961 GCTGCTTACTCTACTTTCGGATAAACCGGAGAACAACTCGGCTTCCAGCATTTTGTGTCGAAGAGGACATTAATGTTGCAGCTCTTGGCAAGCAGCAGCTGAGAATATCTCGAACCC
1321 A A Y S Y F R I N R T I G F Q H F E S E E D I N V A A L G K Q Q P E N I S N P

4081 TTGATGAGAGACCAACTCAGCTCCCCAGAACCTTCTCAGACCCCTTCAAGGACTCTGAAGAACCGGAGCTGTAGGCAATGACCCCTTGAGGACCTGTGAGGCGCTGGACGGGAG
1361 L Y E S T T S A P P E P S Y D D P F T D S E E R Q L E G N D P L R T L * (1394aa)

4201 ATGCCAGCATCACTCACTGCCACCTGGGCACTCAACTGTAATCTCAGCAGCAAGTGGCTTTTAGGAACGTTAAAGTCTTTAAGCACTCAGAAGCCATACCTCATCTCTCTGGCTGAT
4231 CTGGGGTGT

hHARE	1	IQYNLANAIEAADAYTVFAP	NNNAIENIYIREKKVLSLEED	VLRYHVVLVEEKLKNDLHNG	MHRETMGLGFSYFLSFFLHND	OLYVNEAPIYTNVATDKGV
rHARE	23	IHYNLASAIESADAYTVFVP	NNEAIENIYIREKKATSLKED	ILRYHVVLVEEKLKNDLHNG	MHRETMGLGFSYLLAFLRND	OLYVNEAPIYTNVATDKGV
hHARE	101	IHGKGVLEIQKWR	DNMDA	TIIRGRRTSSELT	PFGET	KSLGNEKRR
rHARE	123	IHGKGVLEIQKWR	DNMDA	IIVRGE	GK	SOQAP
hHARE	201	NGGICLDGVNGTGV	E	GEG	ET	TEGKYGIH
rHARE	222	GTASVWDGVNGTGV	Q	GLG	ET	TEGKYGIH
hHARE	301	AAGFQNGTGV	TAI	TAI	TAI	TAI
rHARE	322	AAGFRNGTGV	TAI	TAI	TAI	TAI
hHARE	401	VLTNKG	SEFAL	NET	Q	VERT
rHARE	422	VLTNKG	SPFAL	NET	Q	DORI
hHARE	501	VLRYHVVA	HQLLLENKLI	SNATSLQGEPIVIVSQSTV	FINNEAKVLSDDIISTNGIV	YINNAKIISSDIISTNGIV
rHARE	522	VLRYHVVG	QQLLDNLKVT	TSATTLQGEVPVSVSQSTV	FINNEAKVLSDDIISTNGIV	YINNAKIISSDIISTNGIV
hHARE	601	NLIQDSGLLSVITDPIHTPV	TLFWPTDQALHALPAEQQDF	LFNQDNKDKLKEYLKEHVIR	DAKVLAVDLPTSTAWKTLOG	SELSVK
rHARE	622	KLIQDSGLLSVITDPIHTPV	TLFWPTDQALHALPAEQQDF	LFNQDNKDKLKEYLKEHVIR	DAKVLAVDLPTSTAWKTLOG	SELSVK
hHARE	701	QTRIVQRELLFDLGVAVGI	D	LLIDPTLGR	DTFTTFD	ASGE
rHARE	722	QTRIVQRELLFDLGVAVGI	D	LLMNPTLGR	DTFTTFD	IPGE
hHARE	800	RDQA	PGGPDAP	NNRGV	LDQYSATGE	K
rHARE	822	PDQA	PGGPDTP	NNRGM	RDLYTPMGQ	L
hHARE	900	AHAT	KENNT	E	NLDVEGD	GIT
rHARE	922	VHAT	TENNT	V	NLDVEGD	GIT
hHARE	1000	YVGDGLN	EPEQLPIDR	LQ	DNGQ	HADAK
rHARE	1022	YVGDGLN	EPEQLPLDR	LQ	DNGQ	HPDAS
hHARE	1100	PTAFASQN	SGVVGIVDYG	PRPKSEMWDVF	YRMKDVM	PRPKSEMWDVF
rHARE	1122	PTTYASQN	GANVVGIVDYG	SRPKSEMWDVF	YRMKDVM	SRPKSEMWDVF
hHARE	1200	LFVPQNSGLGENETLSGRDI	EHHLANVSMFFYNLDLVNGT	EHHLANVSMFFYNLDLVNGT	EHHLANVSMFFYNLDLVNGT	EHHLANVSMFFYNLDLVNGT
rHARE	1222	LFVPQNSGLPGNKSLSGRDI	EHHLTNVNVSVFYNDLVNGT	EHHLTNVNVSVFYNDLVNGT	EHHLTNVNVSVFYNDLVNGT	EHHLTNVNVSVFYNDLVNGT
hHARE	1300	HTGLGAGIFFAIIIVTGAVA	LAAYSYFRINRRRTIGFOHFE	LAAYSYFRINRRRTIGFOHFE	LAAYSYFRINRRRTIGFOHFE	LAAYSYFRINRRRTIGFOHFE
rHARE	1321	HSLGTGIFCAVVLVTGAIA	LAAYSYFRIKORTIGFORFD	LAAYSYFRIKORTIGFORFD	LAAYSYFRIKORTIGFORFD	LAAYSYFRIKORTIGFORFD
rHARE	1421	SQOATTVTVPR				

Figure 36

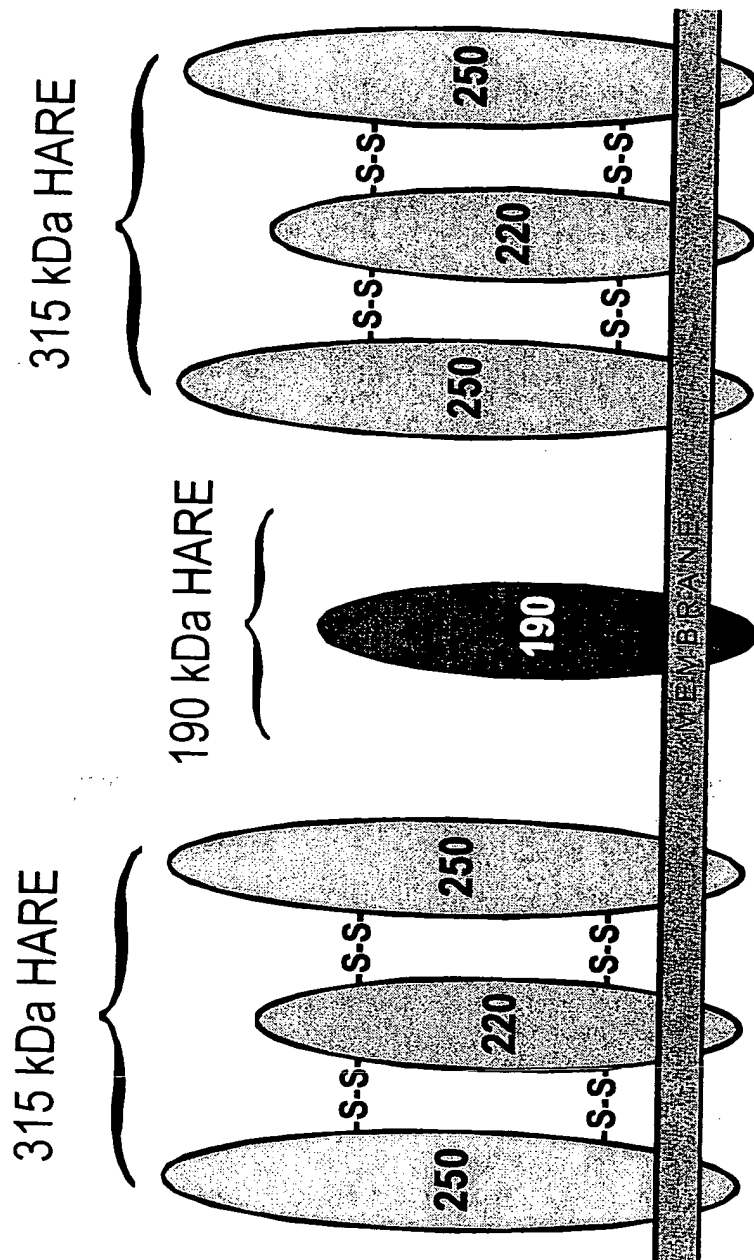
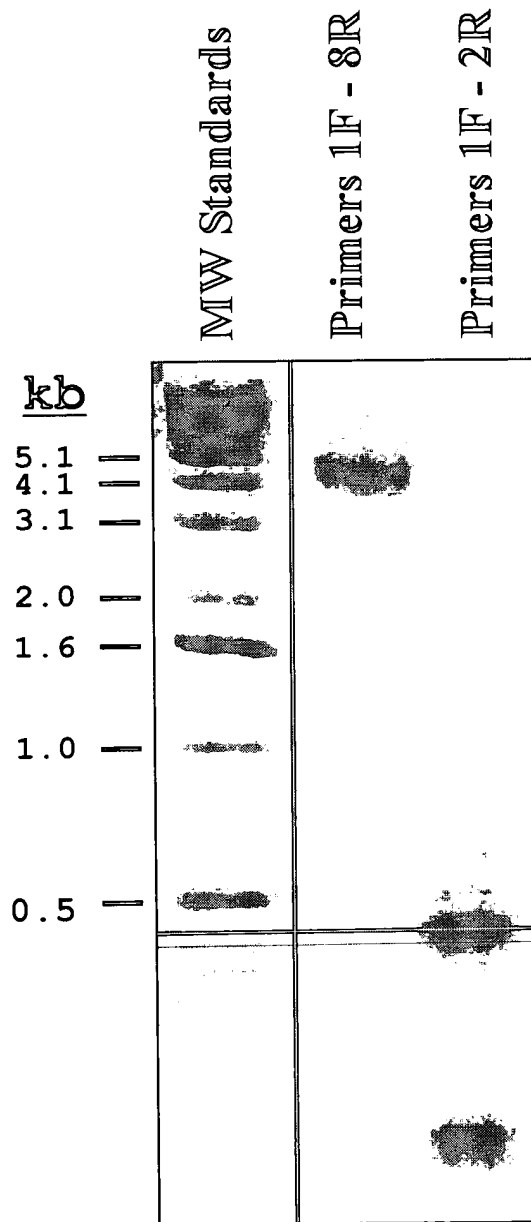


Figure 37

Amplification of the 1394 amino acid HARE
Open Reading Frame from a human lymph
node cDNA Library



105240 02624860

Figure 38

Schematic Organization of the Human HARE Gene on Chromosome 12
(encoding 1357 of the 1394 amino acids disclosed here)

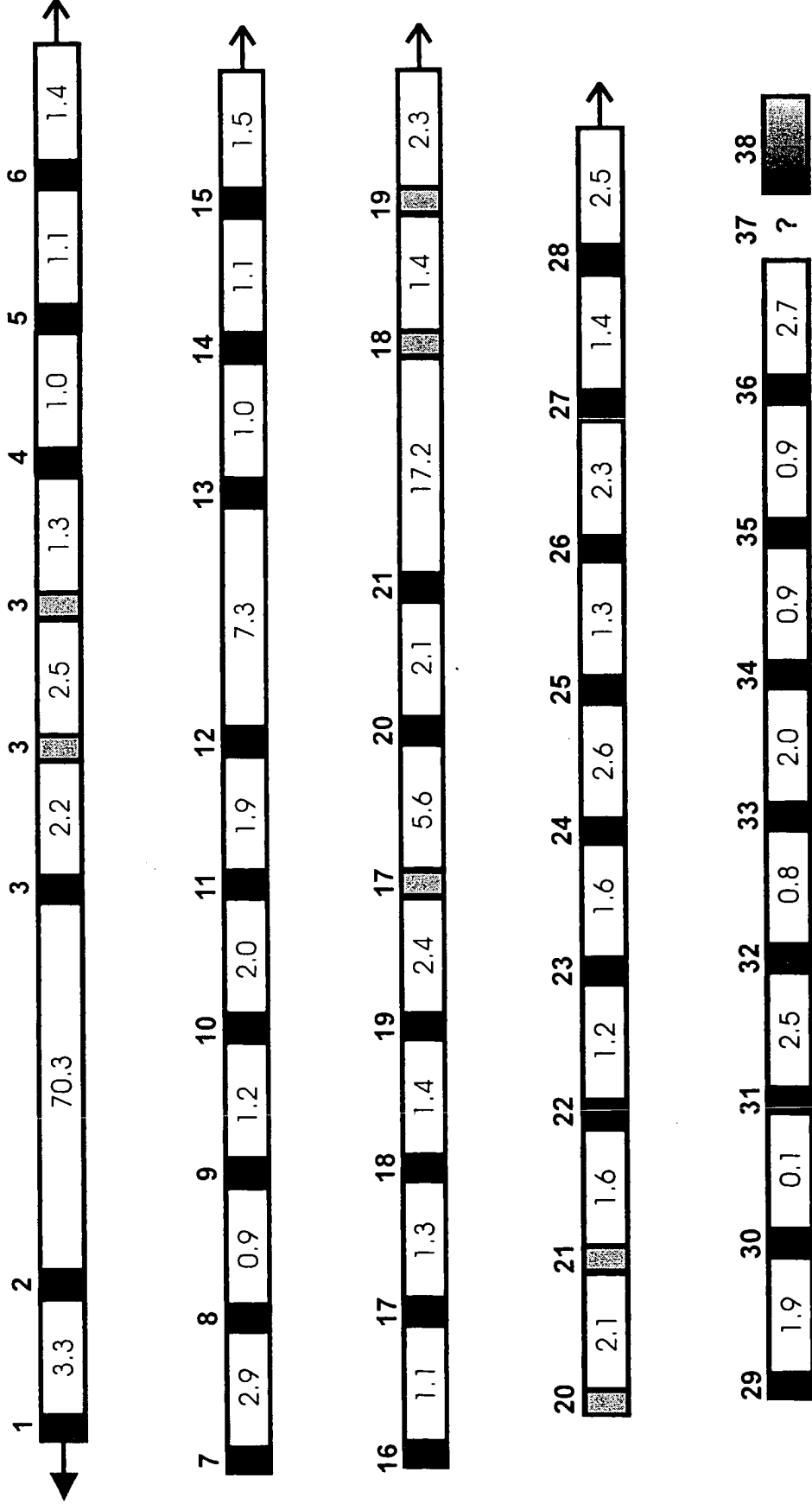


Figure 3 9

